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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein -
                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                             Score
                   1000
997
996
996
991
                                                                                                                     1002
1000
1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A_Geneseq_032802:*
1: /SIDS1/gcgdata/hc
2: /SIDS1/gcgdata/hc
3: /SIDS1/gcgdata/hc
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100.0
99.5
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3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA198.DAT: *
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA198.DAT: *
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA198.DAT: *
10: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
14: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
15: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
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17: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
19: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
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  AAW36047
AAY05531
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AAW97394
AAW61391
AAW97391
AAW97393
AAY05533
                                                                                                                                                              AAY05530
AAW61392
AAW97392
                                                                                                                                                                                                                                                                                                             SUMMARIES
                                      Human bcl-y protei
The human bcl-y pr
Human bcl-w protei
Mouse Bcl-w protei
Mouse Bcl-w protei
Human Bcl-w protei
Human bcl-y pr
Rat bcl-y protein
The rat bcl-y prot
                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                         Human Bcl-w protei
                         Protein
        Bcl-w
                           sequence o
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Apoptosis-biocking	AAW01019	17	232	40.6		45
LED-BCI-XL apoptos	AAU00222	22	485	40.8		44
Human bcl proto-o	N	19	272		0	43
BCT~2	AAB50537	22	239		410.5	42
BCL-2 proce	AAB48288	22	239		10	41
bc1-zaipna.	AAB74129	22	239	40.8	0	40
Human Bcl-2 proter	AAG64036	22	239		0	39
Bc1-2 prote	AAG64035	22	239	40.8		ა 8
2 proce	AAE08573	22	239			37
an BCI-	AAW87812	20	239	40.8	410.5	36
	AAW40217	19	239			ა 5
a L	AAR71404	16	239			34
, ~	AAR70331	16	239			ω ω
ene pr	AAR42312	14	239			32
ce of pcr	AAP80987	9	239	40.8		31
CT-2	AAB35130	22	239	٠		30
bcl-2.	AAB74127	22	239	•		29
an BCI-2	AAW87810	20	239			28
CT-2.	AAB35131	22	236	41.0	41	27
3c1-2 pro	AAG64037	22	239		9	26
BCI-XL	AAB73304	22	233			25
KIM	AAW19396	18	225		4	24
Ö	AAB47515	22	233			23
	AAB50538	22	233		8	22
Rat wild-type BC1-	AAB73303	22	233	42.6	σ.	21
	AAG64262	22	233	•	ω.	20
	AAY69969	21	233	•		19
	AAY83223	21	233	•		18
	AAW31530	18	233	٠	œ	17
Bc1-XL protein. H	AAW05821	17	233	•		16
chymus BCL-	AAR68887	16	233	•	ъ.	15
Bci-XL-DTR apoptos	AAU00219	22	411	43.0	ω.	14
Amino acid sequenc	AAW59884	19	365	76.1	766	13
	AAW36048	18	168	86.1	σ	12

ALIGNMENTS

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AAY05530
                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                             05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                 AAY05530;
                                                                                                                                                                                                                                                                                                    AAY05530 standard; Protein; 193 AA.
                                                                                                                                                                                                                      Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                          Human Bcl-w protein essential for spermatogenesis.
                 An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                               animal model.
                                               WPI; 1999-243890/20.
N-PSDB; AAX25132.
                                                                           Adams J,
                                                                                             (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                 16-SEP-1997;
                                                                                                                                   16-SEP-1998;
                                                                                                                                                      25-MAR-1999
                                                                                                                                                                         WO9913710-A1
                                                                                                                                                                                            Homo sapiens
                                                                          Cory S, Gibson L,
                                                                                                                 97AU-0009228
                                                                                                                                    98WO-AU00764.
                                                                           Koentgen F, Print C;
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Claim 2; Page 33; 52pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Nucleic acids encoding B-cell lymphoma-y protein - useful for
                                                                             Guastella J;
                                                                                                                                      23-FEB-1996;
11-FEB-1997;
                                     N-PSDB;
                                                 WPI; 1998-446079/38.
                                                                                                         (COCE-) COCENSYS INC
                                                                                                                                                                                  11-FEB-1997;
                                                                                                                                                                                                              04-AUG-1998.
                                                                                                                                                                                                                                           US5789201-A
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                   bcl-y; bcl-2;
                                                                                                                                                                                                                                                                                                                             Human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                         02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           AAW61392;
                                                                                                                                                                                                                                                                                                                                                                                                                  AAW61392 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is human Bcl-w, Bcl-2 family which is within.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193;
                                     AAV28334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
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                                                                                                                                                                                                                                                                                              cell death pathway; apoptotic; apoptosis; human.
                                                                                                                                     96US-0012201.
97US-0798897.
                                                                                                                                                                                97US-0798897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                    193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 193;
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Best Local
                                                                                                                                                                                                                                             23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                           Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                            (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5883229-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW97392 standard; Protein; 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Column 17/18; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 galvtvgaffask 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                        96US-0012201.
97US-0798897.
97US-0978523.
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Pred. No. 9.3e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Best Local
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N-PSDB; AAX15946.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel bcl-y homologues of the rat and human bcl-2 protein \, - useful for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cause cell death in, and hence control, parasites.
                                                                                                                                                                                               Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                22-APR-1998
                                                                                                                                                                                                                                                                                                                 AAW36047;
                                                                                                                                                                                                                                                                                                                                                    AAW36047 standard; Protein; 193 AA
   27-MAR-1996;
                                                                                                             WO9735971-A1
                                                                                                                                                Homo sapiens
                                                                                                                                                                                  diagnosis; degenerative
                                                                                                                                                                                                                                        Human bcl-w protein.
                                       27-MAR-1997;
                                                                            02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                              181 galvtvgaffask 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                                                                              (first entry)
                                       97WO-AU00199
   96AU-0008965
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Pred. No. 9.3e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bcl-2 gene family and extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's diseases, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. In the control of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-489635/45.
N-PSDB; AAT96577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a novel human protein, bcl-w, encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 48; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody production or screening of potential modulators.
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                                                                                                                                                     Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                         05-JUL-1999
                                                                                                                                                                                                                                                            AAY05531 standard; Protein; 193 AA
                                                                                                                Mus sp.
                                                                                                                                         animal model.
                                                                                                                                                                                Mouse Bcl-w protein essential for spermatogenesis.
            16-SEP-1997;
                                     16-SEP-1998;
                                                              25-MAR-1999
                                                                                       WO9913710-A1
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                                                                                                                                                                                                                                                                                                                                          GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AA;
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             97AU-0009228
                                     98WO-AU00764.
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99.0%;
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Pred. No. 1.6e-102;
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RESULT
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                                                                                                            WO9913710-A1
                                                                                                                                                                                                                                                 Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                                                                       Human Bcl-w protein essential for spermatogenesis.
16-SEP-1998;
                                                         25-MAR-1999
                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                               animal model
                                                                                                                                                                                                                                                                                                                                                                             05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bel-w gene (see AAX25132-35) or in a gene associated with bel-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise including the sequences capable of inducing.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY05532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY05532 standard; Protein; 193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         facilitating spermatogenesis in animals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 matpastpdtralvadfvgyklrgkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MATPASAPDTRALVADFVGYKLROKGYVCGAGPGEGPAADPLHOAMRAAGDEFETRERRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       galvtvgaffask 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-243890/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
98WO-AU00764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1000; DB 20;
Pred. No. 1.6e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is described of a derivative of human Bcl-w
(see also AAV05530), a pro-survival member of the Bcl-2 family that
is widely expressed and which is essential for spermatogenesis.
The invention relates generally to a method of treatment and to an
animal model for the identification of molecules and genetic
sequences useful for inducing or reducing fertility of male animals.
Methods are provided for the treatment of infertility, or for
reducing fertility, by modulating spermatogenesis. An animal model
carries a mutation is at least one allele of the human or murine
bel-w gene (see AAX25132-35) or in a gene associated with bcl-w.
Such animals have disorganised seminferous tubules and are
substantially infertile, but possess no other major abnormalities
as determined by histological examination. They can be used to
screen for therapeutic molecules including genetic sequences
capable of inducing, enhancing or otherwise facilitating
spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                  Mammalian bcl-y protein.
                                                                                                                                                     20-MAY-1999
                                                                                                                                                                                    AAW97394;
                                                                                                                                                                                                            AAW97394 standard; Protein; 192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                        181 GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 37; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein associated with Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An animal model exhibiting reduced levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX25134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HALL-) HALL INST MEDICAL RES WALTER & ELIZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                              QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                        {	t matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60}
                                                                                                                                                                                                                                                                                         galvtvgaffask 193
                                                                                                                                                                                                                                                                                                                                                  qvqewmvayletrlvdwihssggwaeftalygdgaleearrlregnwasvrtvltgaval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gibson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.38;
99.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1000; DB 20;
Pred. No. 1.6e-102;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koentgen F, Print C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death;

aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;

Kaposi's sarcoma;

lung

cancer;

hyperimmune

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                         RESULT
            AAW61391
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11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                 degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5883229-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). they and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer; Disease, neural and muscular from: strokes, head trauma, Alzheimer; Disease, neural and muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a mammalian bcy-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Columns 19-22; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel bc1-y homologues of the rat and human bc1-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    control, parasites
AAW61391 standard; Protein; 193 AA.
                                                                                                                             181 alvtvgaffask 192
                                                                                                     182 ALVTVGAFFASK 193
                                                                                                                                                                                            61
                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                   8
                                                                                                                                                                                         SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
                                                                                                                                                                                                                                                                                                                   191;
                                                                                                                                                                                                                                                                                                                                                                                            192 AA;
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0012201.
97US-0798897.
97US-0978523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0978523.
                                                                                                                                                                                                                                                                                                                                  99.0%;
99.5%;
                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                  Score 997; DB 20; Length 192; Pred. No. 3.3e-102;
                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                 Qy
                                                                   AAW97391
                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                   Matches 190;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW61391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat bcl-y protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. antisense constructs can be used in disorders where prevention of c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5789201-A
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The mammalian bcl-y protein is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Fig 3A; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-446079/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 death is desired.
                                                     AAW97391 standard; Protein; 193 AA.
20-MAY-1999
                            AAW97391;
                                                                                                                         181 galvtvgaffask 193
                                                                                                                                                                             121 QVQEWMYAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                     181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                              61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                         1\ \mathtt{matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt}
                                                                                                                                                                                                                                                                                                       1 MATDASAPDTRALVADEVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRT 60
                                                                                  9
                                                                                                                                                                                                                                    fs dlaaq lhvtp gs aqqrftqvs delfqggpnwgrlvaffvfgaal caesvnke \texttt{meplvg}
                                                                                                                                                                                                                                                  попопольный выпольный попольный выбучай
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V283333
                                                                                                                                                                                                                                                                                                                                                                                                                         193 AA;
                                                                                                                                                                                                                                                                                                                                                 Conservative
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0012201.
97US-0798897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0798897
                                                                                                                                                                                                                                                                                                                                                                   98.9%;

    Mismatches

                                                                                                                                                                                                                                                                                                                                                      Score 996; DB 19; Length 1
Pred. No. 4.3e-102;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Length 193;
                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                            Gaps
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The rat bcl-y protein.

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В
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                                                                                                                                                                                                                                                                                                                         The present sequence represents rat bcl-y protein (Rbcl-y). The CC specification also describes human bcl-y protein (Rbcl-y). Rbcl-y and CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y and CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y CC proteins may be used to treat conditions associated with a disruption of CC used in therapies to treat subjects suffering from: strokes, head trauma, CC (especially multiple sclerosis), myocardial infarction, vitally induced CC (especially multiple sclerosis), myocardial infarction, vitally induced CC cell death, aging, spinal cord injuries and amyotrophic lateral CC result of triggers which may or may not be apparent. They may also be CC used in this way to develop cell lines which remain viable in culture for CC an extended period. In contrast, if they act as cell death stimulators, CC prolonged cell life span such as cancer (especially kaposi's sarcoma and CC cause cell death in, and hence control, parasites.
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                 121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Columns 15-18; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel bcl-y homologues of the rat and human bcl-2 protein for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX15945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardisease; haraction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                   61
                                                                                     61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parasite.
                                                                                                                                     1 matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                        1 MATPASAPDTRALVADEVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
qvqdwmvtyletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval 180
                                                                  fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120
              Mittinamariamitainiainiamaniamitanama
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                                                                                                                                                         1999-214150/18
                                                                                                                                                                                                                                     h 98.9%;
Similarity 98.4%;
                                                                                                                                                                                                                                                                                                              193 AA;
                                                                                                                                                                                                                        Conservative
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97US-0798897.
97US-0978523.
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                                                                                                                                                                                                                                Score 996; DB 20;
Pred. No. 4.3e-102;
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                                                                                                                                                                                                                                                Length 193;
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Matches 189; Query Match Best Local (

Conservative

1; Mismatches

0 Gaps

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Score 991; DB 20; Length 192; Pred. No. 1.5e-101;

Local Similarity

98.4%; 98.4%;

Sequence

192 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence
                                                                                                                                                                                          The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular demonstrative diseases (associative multiple sclerosis).
                                                                                                                                                                                                                                                                                                                                                            Disclosure; Columns 19-20; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                           Novel bel-y homologues of the rat and human bel-2 protein - useful for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke, head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-1996;
11-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein sequence of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW97393 standard; Protein; 192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW97393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 galvtvgaffask 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GALVTVGAFFASK 193
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97US-0798897.
97US-0978523.
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AAY05533
                                       The present sequence is described of a derivative of mouse Bcl-w (see also AAY05531), a pro-survival member of the Bcl-2 family that CC (see also AAY05531), a pro-survival member of the Bcl-2 family that CC is widely expressed and which is essential for spermatogenesis.

CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.

CC animal model for the identification of molecules and genetic companies useful for inducing or reducing fertility of male animals.

CC sequences useful for inducing or reducing fertility or for male animals.

CC reducing fertility, by modulating spermatogenesis. An animal model CC carries a mutation is at least one allele of the human or murine constant and see animals have disorganised seminferous tubules and are constantially infertile, but possess no other major abnormalities constantially infertile, of the decidences of the decidences in the decidences of the decidence of the decidences of the decidence of the decid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9913710-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein associated with Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX25135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 alvtvgaffask 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 39; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 ALVTVGAFFASK 193
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192 AA;

Query Match

86.1%;

Score 867;

DB 18;

Length 168;

Sequence

168 AA;

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                                  This sequence represents a novel protein, bcl-w, encoded by the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or
                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis; degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW36048;
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                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse bcl-w protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                         Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                             Adams JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                       (AMRA-) AMRAD OPERATIONS PTY LTD.
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                                                                                                                                                                                                 Claim 6; Page 50-51; 86pp; English.
                                                                                                                                                                                                                             degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GALVTVGAFFASK 193
                            screening of potential modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qvqdwivayletrladwihssggwadftalygdgaledarrlregnwa-vstvvtgaval
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                                                                                                                                                                                                                                                                                                                             Cory S, Gibson LM, Holmgreen SP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                 Matches
                                                                          Query Match
                                                                                                                   Sequence
                                                                                                                                 This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                 Claim 1; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                    New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV41925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-1997;
21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (AUCK-) AUCKLAND UNISERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1mmunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW59884 standard; Protein; 365
              1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 qvqdwivayletrladwihssggwadftalygdgaledarrlregnwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 QVQEWMYAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
1998-414099/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mptpastpdtralvadfvgyrlrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MATPASAPDTRALVADFVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120
                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                     Gentz RL,
                                                                                                                  365 AA;
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder; autoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0034205
97US-0034204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US00960
                                          100.08;
                                                                                                                                                                                                                                                                                                                                                                                                     Krissansen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.8%;
                                                                       Score 766;
                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 7e-88;
                                                                                                                                                                                                                                                                                                                                                                                                    GW,
                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Νi J,
                                                         3.1e-76;
                                                                       DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                     Length 365;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                            0,
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                                         Gaps
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                                         0;
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The sequence represents the amino acid sequence of Bcl-Xl-DTR apoptosis-modifying fusion protein comprising Bcl-Xl sequence fused via a short linker to diphtheria toxin receptor binding domain (DTR). The functional apoptosis-modifying fusion protein is capable of binding a target cell and integrating into or crossing a cellular membrane of the target cell. comprising at least two domains, one of which targets the fusion protein to the target cell and another of which modifies an apoptotic response of the target cell. The fusion protein is useful for modifying (inhibiting
                                                                                                                                                                                           Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response
                                                                                                                                                 Claim 4; Page 56-57; 65pp; English.
                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       15-AUG-2000; 2000WO-US22293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W0200112661-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huntington's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bcl-Xl-DTR apoptosis-modifying fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU00219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU00219 standard; Protein; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 qvqewmvayletrladwihssggw 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 QVQEWMVAYLETRLADWIHSSGGW 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fsdlaaq1hvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSDLAAQLHYTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-X1-DTR; apoptosis; cancer; spinal muscular atrophy;
                                                                                                                                                                                                                                                                  AAS00247
                                                                                                                                                                                                                                                                                                                                                              HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                              Liu X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium diptheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           99US-0149220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
254..25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260..41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "DTR, diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Linker amino acids, linking Bcl-xl to diphtheria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "10x histidine tag"
                                                                                                                                                                                                                                                                                                              Collier RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Bcl-X1 amino acids 1 to 233"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            toxin receptor binding domain (DTR)"
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RESULT :
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or enhancing) apoptosis in a target cell, such as neuron, lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or hyperproliferative cell or an adipocyte. It is also useful for reducing apoptosis in a subject after transient ischaemic neuronal injury, especially spinal cord injury. The fusion protein may be used to treat various diseases and injury conditions through inhibition or enhancement of apoptotic cellular response, including neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, spinal muscular atrophy, stroke episodes and unregulated cell growth as in tumours and various cancers. The apoptosis modifying fusion protein can be delivered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              effectively throughout the body and targeted to selective tissue and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                         05-JAN-1995.
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                            multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                            BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease; autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                     Human thymus BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                  10-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR68887 standard; Protein;
New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. neuronal cells, lymphocytes and cancers
                                                                                                                                                                                                                           22-JUN-1994;
                                                                                                                                                (ARCH-) ARCH DEV CORP. (UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGALVTVGAFFAS 192
                                                                            N-PSDB; AAQ81698.
                                                                                            WPI; 1995-052079/07.
                                                                                                                       Boise LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 ngatahsssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgtayqsfeq 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 relvvdflsyklsqkgyswsqfsdveenrteapegtesemetpsaingnpswhladspav 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 RALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 D-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 39.9
93; Conservative
                                                                                                                       Nunez G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                93US-0081448
                                                                                                                                                                                                                           94WO-US07089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.0%;
                                                                                                                       Thompson CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 433.5; DB 2
Pred. No. 2.5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----VCGAGP----GEGPAA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
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                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                      This protein may be expressed recombinantly, particularly with pcmV plasmids as vectors for expression in mammalian cell cultures. The protein has particular application in cancer cells (failure of programmed cell death (PCD)) or neurodegenerative and autoimmune diseases (premature PCD), e.g. Parkinson's disease, amylotrophic lateral sclerosis and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 94; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                          Sequence
185 nggwdtfvelygnnaaaesrkgqerfnrwfltgmtvagvvllgsl 229
                                 141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
                                                                                                                                          29
                                                                                                                                                                                                                                                11 RALVADEVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                           6\ \ relvvdflsyklsqkgyswsqfsdveenrteapegtesemetps ain gnpswhladspav
                                                                                                                                                                           CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                     gvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndhlepwiqe 184
                                                                                                                                                                                                                                                                                      93;
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                          233 AA;
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                      42.6%;
                                                                                                                                                                                                                                                                                       22; Mismatches
                                                                                                                                                                                                                                                                                                      Score 428.5; DB 1
Pred. No. 4.1e-39;
                                                                                                                                                                                                                                                                                                                         DB 16; Length 233;
                                                                                                                                                                                                                                                                                         57; Indels
                                                                                                                                                                                                                                                          ----- V 28
                                                                                                                                                                                                                                                                                           53; Gaps
                                                                                                                                                                                                                        65
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4;

Search completed: June 10, 2002, 10:25:47 Job time: 160 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

Title:
Perfect score:
1007
Sequence:
1 MATPASAPDTRALVADFVGY......LTGAVALGALVTVGAFFASK 193

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:
283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:
283138

Minimum DB seq length: 0
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	æ	7	σ	ъ	4	ω	ພ	1	Result
146.5	146.5	149.5	150	150	153	157.5	173	174	176	182	277.5	346	349.5	356	375.5	377.5	378	403	404.5	406	407	412	412.5	414	423.5	424.5	428.5	428.5	Score
14.5	14.5	14.8					17.2	17.3	17.5		27.6				37.3		•		40.2		•	•	•	•	•	42.2	•	42.6	Query Match
218	179	133	280	261	192	192	211	176	211	170	154	205	199	216	227	214	190	236	233	236	236	236	239	232	233	233	233	233	Length
N	N	N	ν	N	N	2	N	Ν	2	N	N	۲	₽	N	2	2	N	N	N	ы	N	ν	Ľ	N	Ν	2	N	2	DB
B47538	JC7255	153295	A53189	н88578	A47538	D47538	S58875	167435	S58873	I49055	158194	TVHUB1	TVMSB1	B37332	JE0203	149057	A47537	JC7383	167431	TVMSA1	I53744	167432	TVHUA1	S24390	A37332	S51761	B47537	I49056	ID
bcl-2-associated p	Bax-delta protein		apoptosis suppress		~	bcl-2-associated p	cdn-2 protein - hu	cl-xshort		bcl-x short - mous	gene bcl-2 protein	formin				bcl-x transmembran	apoptosis regulato	B-cell lymphoma 2	BCL-X-Long - rat	ng	gene bcl-2 protein		щ		transforming prote	tein	apoptosis regulato	LD.	Description

apoptosis regulator bcl-xL - human N; Alternate names: bcl-2-related protein

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
81.5	82.5	82.5	83	84.5	85	85	87	89	91.5	105	112	118	137.5	141	143
8.1	8.2	8.2	8.2	8.4	8.4	8.4	8.6	8.8	9.1	10.4	11.1	11.7	13.7	14.0	14.2
354	3432	1440	417	358	279	270	3433	185	301	172	350	175	143	255	177
Ν	۳	_	N	ب	N	N	<u>_</u>	N	ν	N	N	N	N	N	Ν
S52040	GNWVJE	GNWVJF	T39939	AJLCQB	В97381	AI2598	GNWVKV	В83217	T36534	I49449	A47476	139055	138921	JC7567	S54778
Gln 1.1 protein -	genome polyprotein	genome polyprotein	DNA binding protei	glutamateammonia	dihydrodipicolinat	dihydrodipicolinat	genome polyprotein	hypothetical prote	probable lipase/es	hemopoietic-specif	BCL2 homolog MCL1	Bci-2 related - hu	bcl-2-associated p	Mcl-la protein - z	NR-13 protein - qu

ALIGNMENTS

RESULT I49056

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A;Experimenta: 551762
A;Accession: 551762
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125,189-233 <N12>
A;Cross-references: EMBL:x82537; NID:g607176;
A;Cross-references: embryonic; brain
                                                                A;Experimental source: em A;Note: smaller form due C;Genetics:
A; Introns: 125/3
C; Superfamily: bcl transforming protein
                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <MIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C;Accession: S51761; S51762
R;Michaelidis, T.M.
                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g607177 A;Experimental source: embryonic; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, November 1994 A; Reference number: S51761
                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S51761
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C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; apoptosis
E;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
E;1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.; Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic A;Reference number: A47537; MUID:93364977
A;Recession: B47537
A;Accession: B47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL-X protein - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-69, 'G', 71-125, 189-233 <BO2>
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A; Residues: 1-233 <BOI>
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C;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Ju1-1999
C;Accession: B47537; C47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB:BCL2L
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 D------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 RALVADFVGYKLRQKGY-----GEGPAA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
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40.6%; Pred. No. 2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
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                                                                                                                                         PIDN:CAA57887.1; PID:g607178
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transforming protein (Bc1-2) homolog - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
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C;Keywords: mitochondrion; transforming protein; transmembrane protein
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C;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997
C;Accession: A37332; S35453
R;Eguchl, Y; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
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A; Residues: 1-233 <EGU>
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                                                                                                                                                    190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK
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                                                                                                                                                                                                                                                                                                                 70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 GWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 VNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 LVADFVGYKLRQKGY------
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                                                                                                                                                                                           AEFTALYGDGALEEARRLREGNWASYRTYLTGAVALGALYTYGAFFASK 193
                                                                                                                                                                                                                                     ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW
                                                                                                                                                                                                                                                                                                                                                                                                  DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69
                                                                                                                                                                                                                                                                          ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSG 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87;
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38.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 423.5; DB 2
Pred. No. 8.4e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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R;Cazals-Hatem, D.L.; Louie, Riochim. Biophys. Acta 1132,

D.C.; Tanaka, 109-113, 1992

S.; Reed, J.C

C; Accession: S24390

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A; Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue A; Reference number: S24390; MUID:92379084
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C;Keywords: mitochondrion; transmembrane protein
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A; Residues: 1-232 <CAZ>
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Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 15-Oct-1999
C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: this report is a correction R;Tsujimoto, Y.; Croce, C.M. Proc. Natl. Acad. Scl. U.S.A. 83, 5214-5218, 1986 Proc. Natl. Acad. Scl. U.S.A. 83, 5214-5218, and protein products of bcl-2, the gene A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene A;Reference number: A29409; MUID:86259760 A;Accession: A29409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transforming protein bcl-2, splice form alpha - human
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A; Residues: 1-95,'A',97-109,'G',111-236,'S',238-239 <TSU>
A; Cross-references: GB:M13994; NID:g179366; PIDN:AAA51813.1; PID:g179367
A; Note: this sequence has been corrected in reference A37332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-239 <EGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown; not compared with conceptual translation
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A;Molecule type: mRNA
A;Residues: 1-58,'T',60-116,'R',118-239 <CLE>
A;Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
A;Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakhshi, A. Oncogene Res. 2, 263-275, 1988
                                                                                                                                                                                                                    R;Cleary, M.L.; Smith, S.D.; Sklar, J. Cell 47, 19-28, 1986
A;Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunogl
                                                                                                                                                                                                                                                                                                                                                                              A;Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-A;Reference number: S02452; MUID:88196071
A;Accession: S02452
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                                                                                                                                                                               A; Reference number: A24428; MUID:87002488
                                                                                                                                                                                                                                                                                                                     A; Residues:
                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                          A; Accession: A24428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 LFRDGVNWVRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWD 189
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                                                                                                                                                                                                                                                                                                                         1-239 <SET>
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A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphom A;Reference number: A27622; MUID:88217344
A;Accession: A27622
A;Molecule type: mRNA
A;Residues: 1-58,77,60-239 <HUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:119031; OMIM:151430
A;Map position: 18q21.3-18q21.3
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A;Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
A;Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
A;Note: the sequence was determined from the germline gene
C;Comment: Constitutive expression of BCL2 following t(14:18) chromosomal translocati
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                                                                                                                                                                                                                                                                                                                                                                                      R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid
A;Reference number: I53295; MUID:95129487
A;Accession: I67432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: 167432
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A; Cross-references: EMBL: U34964; NID: g1
C; Superfamily: bcl transforming protein
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    rat (fragment)

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                                                   10 DNRETVMKYIHYKLSQRGYEWDTGDEDSAPLRRAPTPGIFSFQPESNRTPAVHRDTAART 69
                                                                                                                                                                        Local
                                                                                                   9 DTRALVADFVGYKLRQKGY-----
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----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
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                                                                                                                                                   84;
                                                                                                                                                                          Similarity
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37.0%; Pred. No. 9e-
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                                                                                                                                                                             Score 412; DB 2;
Pred. No. 9.9e-31;
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A;Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109 R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y. Nucleic Acids Res. 20, 4187-4192, 1992 A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a 'A;Reference number: A37332; MUID:92375724 A;A;Accession: E37332
                                          A;Molecule type: DNA
A;Residues: 1-33,'E',34-220,'AL',223-236 <EGU>
C;Genetics:
                                                                                                   A: Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                          R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homo:
A;Reference number: A90893; MUID:87187643
                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
C;Accession: A25960; E37332
                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-236 < NEG>
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A:Title: Cloning and sequencing of a cDNA encoding the A:Reference number: I53744; MUID:94193015
A:Accession: I53744
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May_1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
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A; Residues: 1-236 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 40.4%; Local Similarity 35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T.; Irie, S.; Krajewski, S.; Reed, J.C. 0, 291-292, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 DTRALVADFVGYKLRQKGY---------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bc1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGWDAFVELYG----PSMRPLFDFSWQSLKTLLSLAL-VGACITLGAYLGHK 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Mismatches
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
.9e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
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                                                                                                   not compared with conceptual
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                                                                                                        tra
                           B-cell lymphoma 2 protein - Chinese hamster
C;Speckes: Cricetulus griseus (Chinese hamster)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000
C;Accession: JC7383
                                                                                                                              JC7383
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R; Tomicic, M.T.; Christmann, M.; Kaina, B.
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R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A:Title: Expression of members of the bcl-2 gene family in
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid
A:Reference number: 153295; MUID:95129487
A:Accession: 167431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: bcl transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-233 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
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C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                           185 NGGWDTFYDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                             141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                         125 QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184
                                                                                                                                                                                                                                                                                                                                                 81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                                                                                                66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                             29 CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 RALVADFVGYKLRQKGY------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELYVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: U34963; NID: g1004376; PIDN: AAA77686.1; PID: g1004377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 404.5; DB 1
Pred. No. 4.8e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 406; DB 1; Pred. No. 3.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                          #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 236;
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the immature

rat ovary: eq

53;

Gaps

4;

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A; Molecule type: mRNA
A; Residues: 1-236 <TOM>
A; Cross-references: GB:AJ271720
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C;Superfamily: bcl transforming protein
C;Keywords: B-cell lymphoma; ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Comment: This protein has anti-apoptotic function, and supports cell survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
A47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents: Ovary
A; Accession: JC7383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A;Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA A;Rosidues: 1-190 <BOI> A;COIS-references: GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1; PID:g510899 C;Superfamily: bcl transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.; Cell 74, 597-608, 1993
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: A47537
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A; Accession: A47537
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watch 40.0%; Score 403; DB 2; Length 236; Local Similarity 35.3%; Pred. No. 6.7e-30; nes 82; Conservative 34; Mismatches 64; Indels
  186 R-TAL 189
                                                146 EFTAL 150
                                                                                      126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART
                                                                                                                                                                                66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125
                                                                                                                                                                                                                                                                                                                         11 RALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                          LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                                                              RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65
                                                                                                                                                                                                                                                                                                                                                                       81;
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 378; DB 2; Length 190; 43.8%; Pred. No. 1.1e-27;
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                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                            -----VCGAGPGEGP-----
                                                                                                                                                                                                                                                                                                                                                                          44; Indels
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bcl-x transmembrane deleted - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
I49057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: bcl-x-long
C;Superfamily: bcl transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-214 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: I49055; MUID:95052604
A; Accession: I49057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: I49057
                                                                                                                                                                                                                                                                                                                                                              R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E. Biophys. Res. Commun. 248, 147-152, 1998
B;Title: Identification of a human cDNA encoding a novel bcl-x isoform. A;Reference number: JE0203; MUID:98340865
A;Accession: JE0203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apoptosis regulator bcl-x isoform - N; Alternate names: h-bcl-xbeta
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JE0203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999
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                                                                                                                                                                                                                    A; Map position: 20 C; Superfamily: bcl transforming protein
                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-227 <BAN>
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QY
                                        B
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                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 RALVADFVGYKLRQKGY------
                                                                              11 RALVADFVGYKLRQKGY------
  29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                          Local Similarity
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                                      RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
                                                                                                                         82;
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                                                                                                                         Conservative
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                                                                                                                    37.3%; Score 375.5; DB 2
40.8%; Pred. No. 2.3e-27;
ative 18; Mismatches 50
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Pred. No. 1.4
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transforming protein (bcl-2-beta) - chicken
C:Species: Gallus gallus (chicken)
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Apr-1998
C;Accession: B37332; S35452
R;Equchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie A;Reference number: A37332; MUID:92375724
A;Accession: B37332
A;Status: nucleic acid sequence not shown
A;Rociduse: 1-216 <EGU>
A;Cross_references: EMBL:D11381; EMBL:D11382
C;Superfamily: bcl transforming protein
Search completed: June 10, 2002, 10:26:22 Job time: 170 sec
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B37332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.4%; Score 356; DB 2; Length 216; Best Local Similarity 38.4%; Pred. No. 1.4e-25; Matches 71; Conservative 21; Mismatches 49; Indels 44; Gaps
                                                                                                                        190 VRACA 194
                                                                                                                                                                                                          130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189
                                                                                                                                                                     145 AEFTA 149
                                                                                                                                                                                                                                           85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                  42 -----LHQAMRAAGDEFETRERRTESDLAAQLHVTPGSAQQRETQVSD 84 :| |:| ||| || |::| ||::| || :| || || :|
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                                                                                                                                                                                                                                                                                                    70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129
                                                                                                                                                                                                                                                                                                                                                                                                 10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAAAAPAAVAAAGASSHHRPEPPGSA 69
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Mon Jun 10 11:32:17 2002

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OM protein - protein search, using sw model
                                                                                                                                          Total number of hits satisfying chosen parameters:
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                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                        Title:
                                    Post-processing: Minimum Match 0%
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                                                                                                                                                                                       105224 seqs, 38719550 residues
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1 MATPASAPDTRALVADEVGY......LTGAVALGALVTVGAFFASK 193
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

SwissProt_40:*

SUMMARIES

1 3 4 4 4 4 4 4 4 4 4 4 4 4 4	Result
1007 1007 646.5 432.5 428.5 428.5 428.5 428.5 428.5 428.5 416.5 416.5 416.5 417.6 177.5 17	Score
100.0 94.3 64.2 42.9 42.6 42.6 42.6 42.6 42.7 41.0	Query Match L
193 1 2193 1 2293 1 2329 1 2333 1 2333 1 2333 1 2333 1 2336 1 236 1 236 1 236 1 236 1 204 1 204 1 211 1 192 1 192 1 192 1 192 1 192 1 193 1 193 1 194 1 195 1 197	Length DB
BCLW_HUMAN BCLW_MOUSE AR1_XENLA BCLX_CHICK BCLX_HUMAN BCLX_AMOTE BCL2_CHICK BCL2_BOVIN BCL2_HUMAN BCL2_HUMAN BCL2_HUMAN BCL2_HUMAN BCL2_HUMAN BCL2_HUMAN BCL2_CHICK BCL2_HUMAN BCL2_CHICM BCL2_HUMAN BCL2_CHICM BAK_HUMAN BAK_HUMAN BAK_HUMAN BAKA_HUMAN BAXA_HUMAN BAXA_HUMAN CED9_CAEBL BAXA_HUMAN RATI BAXA_HUMAN RATI_HUMAN RATI_HUMAN RATI_HUMAN RATI_HUMAN BEL1_HUMAN BEL1_HUMAN BEL1_HUMAN BEL1_HUMAN BEL1_RASFM2 BAR_ASFM2 BAR_ASFM2 BAR_ASFM2 BAR_ASFM2 BAR_ASFM2 BAR_ASFM2	ID
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8. 8 8. 5 8. 2 8. 2 8. 2 7. 8 7. 8
658 3433 358 1440 3432 396 541 3430 886 886 454
SOHC_BRAJA POLG_KUNJM GLNA_LACSA POLG_JAEVJ POLG_JAEVJ POLG_JAEVJ PORA_PYRFU FTCD_RAT POLG_WNV A_DROME TSSP_MOUSE YB48_MYCTU YJ45_MYCTU
p54924 bradyrhizob p14335 k genome po p23712 lactuca sat p14403 j genome po Q51804 pyrococcus O88618 rattus norv p06935 w genome po p14599 drosophila Q9qxe5 mus musculu 006448 mycobacteri p95269 mycobacteri

ALIGNMENTS

	38888	3888888	3000 P	RT RT	RP R	OX COC	DI	RESULT BCLW_H ID B
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). EMBL: U59747; AAB09055.1; EMBL: U597461; BAA19666.1; EMBL: D87461; BAA19666.1; HSSP: Q07817; IMAZ. MIM: 601931; InterPro; IPR002475; BCL2_family. InterPro; IPR003093; BH4.	SWISS-PROT entry is copyright. It is produced through a collaborat ween the Swiss Institute of Bioinformatics and the EMBL outstatic Furopean Bioinformatics Institute. There are no restrictions on	N THE ANTI-APOP AIN 1 (BH1). AIN 2 (BH2). AIN 4 (BH4).	DNA Res. 3:321-339(1996). - I - FUNCTION: PROMOTES CELL SURVIVAL. - I - SUBCELLULAR LOCATION: Cytoplasmic. - I - SUBCELLULAR LOCATION: CYTOPLASMIC. - I - TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND - I - TISSUE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-Brain; TISSUE-Brai	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-96358615; PubMed-8761287; MEDLINE-96358615; PubMed-8761287; MEDLINE-96358615; PubMed-8761287; Medlins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.; "bcl-w, a novel member of the bcl-2 family, promotes cell survival."; "bcl-w, a novel member of the bcl-2 family, promotes cell survival."; "concogene 13:665-675(1996).	Apoptosis regulator bet m. BCLJL2 OR BCIM OR KIAA0271. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)	RESULT 1 BCLW_HUMAN STANDARD; PRT; 193 AA.

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                                                                        ROSS A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K., Russell L.D., Macgregor G.R.;
"Testicular degeneration in Bclw-deficient mice.";
Nat. Genet. 18:251-256(1998).
-i- FUNCTION: PROMOTES CELL SURVIVAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50062; BCL2_FAMILY PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01260; BH4 1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                          MEDLINE=96358615; PubMed=8761287;
Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,
Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;
"bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
                                                                                                                                            STRAIN=C57BL/10J;
MEDLINE=98160183; PubMed=9500547;
                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                       Oncogene 13:665-675(1996).
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          Apoptosis regulator Bcl-W. BCL2L2 OR BCLW.
                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                          BCLW_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                            SUBCELLULAR LOCATION: Cytoplasmic.

TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
  AND SALIVARY GLAND.

DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MATPASAPDTRALVADFVGYKLROKGYVCGAGDGEGPAADPLHQAMRAAGDEFETRERRT 60
 FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 BI
104 BJ
151 BI
; 20774 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH2
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1007; DB 1;
Pred. No. 2.5e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3792243A50281761 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Вþ
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                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                  AR1_XENLA
Q91827;
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TISSUE-Head;
          SEQUENCE FROM N.A.
                                      Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                Amphibia; Batrachia; Anura;
                                                                                                    Apoptosis regulator R1 (XR1) (Fragment).
                                                                                                                    01-NOV-1997 (Rel. 35, Last sequence up 01-NOV-1997 (Rel. 35, Last annotation
                                                                                            Xenopus laevis (African clawed
                                                                                                                                                     01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                 121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00452; Bc1-2; 1. Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                 181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
InterPro; IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U59746; AAB09056.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                    61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEDLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MATPASAPDTRALVADFYGYKLRQKGYYCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                            ω
                                                                                                                                                                                                                                                                                                                                                                                                          1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                  GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                              QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                      FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:108052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF030769; AAB86430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q07817; 1MAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50062; BCL2_FAMILY; 1.
PS01080; BH1; 1.
PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS01260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 AA;
                                                                                                                                                (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                    Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
9
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    вн2; 1.
вн4_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bc1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH4_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 B
104 B
151 B
: 20790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.3%;
99.0%;
                                                          Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1000; DB 1;
Pred. No. 1e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH4.
BH1.
BH2.
36CA185F5945DFB4 CRC64;
                                                                                                                                                                             PRT;
                                                                                            frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                   update)
                                                                                                                                                                            228 AA.
                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell-survival genes.";
Gene 158:171-179(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cruz-Reyes J., Tata J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95331613; PubMed=7607538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning,
                                                                              ECLX_CHICK STANDARD; PRT; 229 AA (Q07816; Q98908; 01-FEB-1995 (Rel. 31, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
Apoptosis regulator Bcl-X. BCL2L1 OR BCLX OR BCL-X. Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130
                                                                                                                                                                                                                                                                                                                                         225
                                                                                                                                                                                                                                                                                                                                                                                             190
                                                                                                                                                                                                                                                                                                                                                                                                                                                 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48
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BEVELOPMENTAL STAGE: DEVYELOPMENTAL REGULATION ONLY OCCURS IN THE BRAIN OF MUD-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRALVEDLVRYKLCORSLV---PEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pro; IPR000712; Bcl_2.
PF00452; Bcl-2; 1.
PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                         FASK 228
                                                                                                                                                                                                                                                                                                                                                                                             FASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X82462; CAA57845.1; -. Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00337; BCL; 1.
SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterization and expression of two Xenopus bcl-2-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR003093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002475; BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 E
227 E
25068 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 646.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 5.7e-51
                                                                                                                                                                                                      229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL-W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on
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Vilagrasa X., Mezquita C., Mezquit
"Differential expression of bcl-2
spermatogenesis.";
Mol. Reprod. Dev. 47:26-29(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (LONG FORM).
STRAIN-HUBBARD WHITE MOUNTAIN; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "bcl-x, a bcl-2-related gene that functions as a dominant regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boise L.H., Gonzalez-Garcia M.,
Turka L.A., Mao X., Nunez G., T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (SHORT FORM). MEDLINE=93364977; PubMed=8358789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97264485; PubMed=9110311;
                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z23110; CAA80657.1; -. EMBL; U26645; AAB07677.1; -. PIR; A47537; A47537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
SEQUENCE
                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                         PROSITE
                                                                                                                                                                                                                                                                                                                                PROSITE
                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003093; BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000712; Bcl_2.
                                                      VARSPLIC
                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptotic cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENVELOPE (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPTOOL DEV. 47:26-29(1997).
FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF02180; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P53563; 1AF3
                                                                                                                                                                                                                                                                                                   PS01080; BH1;
PS01258; BH2;
PS01259; BH3;
                                                                                                                                                                                                                                                  PS01260; BH4_1;
PS50063; BH4_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002475; BCL2_family.
                                                                                                                                                                                                                           Transmembrane;
  229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAA80657.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bcl-2;
                                                         24
96
144
191
223
223
  25733
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     ¥.
                                                                                                                                                                                                                           Alternative splicing
BH2.
POTENTIAL.
ERFYDLYGNNAAAELRKGQETENKWLLTGATVAGVLLLGSL
LSRK -> VRTALP (IN SHORT ISOFORM).
, A97D3A4D04C0E9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thompson C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Postema C.E., Ding L., Lindsten T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and bcl-x during chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE SHORT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G. "Expression of apoptosis-associated genes in hibernating myocardium of pig.",
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Potent inhibitor of cell death. Inhibits a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIG
                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis regulator Bcl-x.
BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCLX_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                      apoptotic activity (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                 DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bc12 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis (By similarity). The cleaved protein, lacking the BH4 domain, has protein and the BH4 domain, has protein.
                                                                                                                                                                                                                                                                                                                                                                                                             SÜBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane.

SUBUNIT: Bcl-x(L) forms heterodiment.
                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ģ
Q07817;
                AJ001203; CAA04597.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFVDLYGNNA---AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE
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1MAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.98;
41.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 432.5; DB 1;
Pred. No. 8.4e-32;
22: Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schulz R., Heusch G., Darmer D.; genes in hibernating and stunned
                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 AA.
                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                       bу
                                                                                       and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Ву
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                                                                                                                                                                                                                                                                                                                                                                                BCLX_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                Boise L.H., Gonzalez-Garcia M., Postema C.E.
Turka L.A., Mao X., Nunez G., Thompson C.B.,
"bcl-x, a bcl-z-related gene that functions
of apoptotic cell death.";
                                                                                                                                                                                                                                                                                                  BCLX_HUMAN STANDARD; PRT; 233 AA Q07817; Q92976; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
    Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise L.H., Thompson C.B.
                                                               Inohara N., Ohta S.;
Submitted (OCT-1996) to
Korsmeyer S.J.;
                       MUTAGENESIS OF GLY-138, AND HETER
MEDLINE-95372373; PubMed-7644501;
                                                                          Inohara N.,
                                                                                       SEQUENCE FROM N.A. (ISOFORM BETA).
                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)). MEDLINE=93364977; PubMed=8358789;
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                Apoptosis regulator Bcl-x. BCL2L1 OR BCL2L OR BCLX.
                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
InterPro; IPR000712; Bc1_2.
Pfam; PF00452; Bc1_2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00337; BCL; 1
SMART; SM00265; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                  185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 RALVADFVGYKLRQKGY-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV
                                                                                                                   74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                              NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVLNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS01259; BH3; 1.
PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50062; BCL2_FAMILY; 1.
PS01080; BH1; 1.
PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210
233 AA;
                                      OF GLY-138, AND HETERODIMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion;
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100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.9%; Score 431.5; DB 1
41.8%; Pred. No. 1.1e-31;
                                                              the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Mismatches
                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                     Postema C.E., Ding L., Lindsten T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18BF6FA0441912B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                               233 AA
                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                           as a dominant regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
[5]
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLEAVAGE BY CASPASES, AND MUTAGENESIS OF MEDILINE-98118550; PubMed=9435230; Clem R.J., Cheng E.H.-Y., Karp C.L., Kirs Takahashi A., Kastan M.B., Griffin D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure of Bcl-xL-Bak peptide complex: recognition between regulators of apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 1-209. MEDLINE=97172562; PubMed=9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Korsmeyer S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ng S.L., Fesik S.W.;
"X-ray and NMR structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY MEDLINE=96256675; PubMed=8692274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Bax-independent inhibition Nature 379:554-556(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGENESIS OF BH1 AND BH2 DOMAINS. MEDLINE=96170038; PubMed=8596636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 381:335-341(1996).
[7]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muchmore S.W., Sattler M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science
                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Modulation of cell death bx Bcl-xL through caspase interaction.";
Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).
-I- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hardwick J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Multiple Bcl-2 family members demonstrate selective dimerizations
                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S) AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.

DOMAIN: The BH4 domain is required for anti-apoptotic activity.

The BH4 and BH2 domains are required for both heterodimerization.
                                                                                                                                                                                                SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoptotic activity.
SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Bcl-x(L) forms het
                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                SIMILARITY:
                                                                                                                                                                                                                                                                                            with other Bcl2 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heterodimerization with BAX does not seem to be required for anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-x(S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENVELOPE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E.H.-Y., Levine B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 92:7834-7838(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nettesheim D., Chang B.S.,
                                                                                                                                                                                BELONGS
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                                                                                                                                                                                TO THE BCL-2 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heterodimers with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thompson C.B., Hardwick J.M.,
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Best Local
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SMART; SM00265; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1
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EMBL;
EMBL;
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3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [nterPro;
185
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1LXL; 21-APR-97
                                                                                                                                                                          CGAGPGEGPAAD-------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
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                                                                                                                                                      NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                     SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                            QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE
                                                                                                QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAXLETRLADWIHS 140
                                                                                                                                                                                                                                    RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
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Z23115; CAA80661.1;
U72398; AAB17354.1;
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PS01080; BH1;
PS01258; BH2;
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BH4_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative
                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G->A: NO HETERODIMERIZATION WITH BAX.
G->E: NO HETERODIMERIZATION WITH BAX.
D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLEAVAGE BY CASPASE-1.

MISSING (IN ISOFORM BCL-X(S)).

DITYVELYGNNAAAESRKGQERENRWFLIGMTVAGVVLLGSL
FSRK -> VRTKPLVCPFSLASGQRSPTALLLYLFLLCWVI
VGDVDS (IN ISOFORM BCL-X(BETA)).
                                                                                                                                                                                                                                                                                                                                   Score 428.5;
Pred. No. 2e
                                                                                                                                                                                                                                                                                                                                                                                                                                 D->A: NO EFECT ON CASPASE-1 CLEAVAGE G -> A (IN REF. 1; CAA80661).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRI->ELN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY ABOUT HALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNW->AIL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRD->VRA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WD->GA: REDUCES ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                 E09D3CDD851AE9BE CRC64;
                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEAVAGE BY CASPASE-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splicing; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOSS OF ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                     2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOSS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO HETERODIMERIZATION WITH
                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                    53;
                                                                                                                                                                                                                                                                             ----- 28
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВУ
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4;

RESULT 7
BCLX_MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic organization, promoter region analysis, and ch
localization of the mouse bcl-x gene.";
J. Immunol. 158:4750-4757(1997).
-!- FUNCTION: Potent inhibitor of cell death. Inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6 X CBA; TISSUE-Thymus; MEDLINE-98051053; PubMed-9390687; Yang X.-F., Weber G.F., Cantor H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCLX_MOUSE STANDARD; PRT; 233 AA 664373; Q60657; Q60658; Q61338; Q1-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thompson C.B., Nunez G.;
"bcl-XL is the major bcl-x mRNA form edevelopment and its product localizes
Development 120:3033-3042(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=97289584; Pubmed=9144489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95052604; PubMed=7963517; Fang W., Rivard J.J., Mueller D.L., Beh. "Cloning and molecular characterization"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis regulator Bcl-x. BCL2L1 OR BCL2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM X(BETA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocytes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS X(L); TISSUE=Pre-B cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gonzalez-Garcia M., Perez-Ballestero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95331139; PubMed=7607090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6; TISSUE=Brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS X(L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kamesaki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-2A4B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mmunity 7:629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel Bcl-x isoform connected to the T cell receptor regulates optosis in T cells ";
       POSTNATAL TISSUES, WHEREAS POSTNATAL TISSUES.

DOMAIN: The BH4 domain is 1
The BH1 and BH2 domains are
                                                                                                                                                                                                                                                                        isoform promotes apoptosis.

SUBUNIT: Bcl-x(L) forms heterodimers with BAX does not seem to be similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity).

SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).

ALTERNATIVE PRODUCTS: 4 ISOFORMS; BCX-X(L) (SHOWN HERE), BCL-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol. 153:4388-4398(1994).
                                                                                                                            TM) EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES ACTIVATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-x(S)
                                                                                                          DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                        BCL-X(BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seldin M.F., Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H., Michaud G.Y., T (MAR-1995) to the
                                                                                                                                                                           SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA-
                                                                                                                                                                                                                                                        AND BCL-X(DELTA-TM); ARE PRODUCED
domain is required for anti-apoptotic activity. domains are required for both heterodimerization
                                                                                                       BCL-X(BETA) IS EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takatsu K., Okuma M.;
e EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                           BCL-X(L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X(S) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Behrens
tion of m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed during murine
s to mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X(BETA)).
                                                                                \mathbf{S}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ding L., Duan L., Boise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse
                                                                                PREDOMINANTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X(DELTA-TM))
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                                                                                                       IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and chromosome
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                                                                                                                                                                                                                                                        BY ALTERNATIVE
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                                                                                FOUND
                                                                                                       EMBRYONAL
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                                                                                                                                                        HAVE BEEN
                                                                                                                                                                                                                                                                           BCL-X(S)
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                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003093; BH4.
InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002
InterPro; IPR003
InterPro; IPR000
Pfam; PF00452; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis;
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: Proteolytically cleaved by caspases during apoptosis similarity). The cleaved protein, lacking the BH4 domain, apoptotic activity (By similarity).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
    125
                                           81
                                                                                      99
                                                                                                                                  29
                                                                                                                                                                                                                    11 RALVADFVGYKLRQKGY----------
                                                                                                                                                                             6
                      QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS
QVVNELERDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                             CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                         RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:88139;
                                                                                      NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U10100;
U51279;
U78031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U10102;
U10101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X83574;
L35049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P53563;
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                                                                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50062; BCL2_
PS01080; BH1;
PS01258; BH2;
PS01259; BH3;
PS01260; BH4_1
PS50063; BH4_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88139; BC121.
IPR002475; BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                             233
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129
129
180
210
126
189
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AAA51039.1;
AAA51040.1;
AAA82174.1;
AAA82173.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1AF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC53460.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA82172.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB96881.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB96881.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCL2_FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
148
195
226
288
233
                                                                                                                                                                                                                                                                                                                                                                             26132
                                                                                                                                                                                                                                                                                      42.6%;
                                                                                                                                                                                                                                                                                                                                                                             W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOINED
                                                                                                                                                                                                                                                                  22; Mismatches
                                                                                                                                                                                                                                                                                    Score 428.5; DB Pred. No. 2e-31;
                                                                                                                                                                                                                                                                                                                                                                         X(DELTA-TM)).
; 24D2AC79887E072E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

MISSING (IN ISOFORM BCL-X(S)).

DTFVDLYGNNAAAESRKGOERENRWFLJGMTVAGVVLLGSL
ESRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL-X(BETA)).
LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK
                                                                                                                                                                                                                                                                                                                                                                                                                    GHDCGWCGSAGLTLQSEVTRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splicing; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                               57;
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                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                    (IN ISOFORM
                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                             Gaps
                                                                                      12
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141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183

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P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128; Q1-QT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-QCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95129487; PubMed=7828536;
Tilly J.L., Tilly K.L., Kenton M.L., Johnson A.L.;
"Expression of members of the bcl-2 gene family in the immature rat
"expression of members of the bcl-2 gene family in the immature rat
ovary: equine chorionic gonadotropin mediated inhibition of granulosa
cell apoptosis is associated with decreased bax and constitutive
bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptosis regulator Bcl-x.
BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ol "An additional form of rat Bcl-x, Bcl-xbeta, generated by an unspliced RNA, promotes apoptosis in promyeloid cells."; J. Biol. Chem. 271:13258-13265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wesselingh S.L., David G.L., Choi S., Veliuona M., Submitted (JUN-1995) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
Michaelidis T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                    the Bcl-2 protein family ;
J. Biol. Chem. 272:27886-27892(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=SPRAGUE-DAWLEY; TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Thymus; MEDLINE=96278736; PubMed=8662675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98010630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aritomi M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal structure of rat Bcl-xL. Implications for the function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
AND BCL-X(BETA); ARE PRODUCED BY ALIFERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
DETECTABLE LEVEL OF BCL-X(S).
DOMAIN: The BH4 domain is required for anti-apoptotic activity.
The BH1 and BH2 domains are required for both heterodimerization
                                                                                                                                                                                Bcl-x(beta) isoforms promote apoptosis.
SUBUNIT: Bcl-x(L) forms heterodiners with BAX, BAK and Bcl-2
similarity). Heterodimerization with BAX does not seem to be
required for anti-apoptotic activity (By similarity).
SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
                                                                                                                                                                                                                                                                                                   FUNCTION: Potent inhibitor of cell death. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator,
                                                                                                                                           ENVELOPE (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S)
                                                                                                                                                                                                                                                                                  cytochrome c, from the mitochondrial membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=9346936;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hardwick J.M.;
                                                                                                                                                                                                                                                                                               The Bcl-x(S) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus.
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                                                                                                          Query Match
Best Local :
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InterPro; IPR003093; BH4.
InterPro; IPR003712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its contenmodified and this statement is not removed. Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                   CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X82537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00337; BCL;
SMART; SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; lAF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis;
                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                               3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with other Bc12 family members and for repression of cell death.

PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH4).
 66
                     29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                      11 RALVADFVGYKLRQKGY------
                                               თ
NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S78284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U10579;
                                               RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion;
                                                                                                                                                         6
12
64
81
119
119
143
199
201
233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; CAA57886.1; -.; CAA57887.1; -.; CAA57887.1; -.; AAA19257.1; -.); AAB17353.1; -.
                                                                                               Conservative
                                                                                                                                                                                                                                                                                              4
86
129
180
180
210
210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC60702.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC60701.1; ALT_INIT.
                                                                                                                                                                                                                                                                                              24
100
148
195
226
188
233
                                                                                                                                                                                                         12
64
81
119
                                                                                                            42.6%;
                                                                                                                                                             26158 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing; Transmembrane;
                                                                                                22; Mismatches
                                                                                                                                                                                                       R -> Q (IN REF. 1
F -> S (IN REF. 2
A -> E (IN REF. 2
I -> L (IN REF. 4
A -> V (IN REF. 4
                                                                                                         Score 428.5; DE
Pred. No. 2e-31;
                                                                                                                                                                                                                                                                                  DTFVDLYGNNAAAESRKGQERENRWELTGMTVAGVVLLGSL
FSRK -> VRTTPLVCPPLVCLSSVETDNCDEWSDCMNVED
                                                                                                                                                                      A -> T (IN REF. 4).
A -> P (IN REF. 4).
                                                                                                                                                                                                                                                                                                        MISSING
                                                                                                                                                                                              FF -> SS
                                                                                                                                                                                                                                                                     IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                           -> P (IN REF. 4).
2B62B6C63864BC8F CRC64;
                                                                                                                                                                                                                                                                                                           (IN ISOFORM BCL-X(S))
                                                                                                                                                                                                 (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no rest
                                                                                                                      DB 1; Length 233;
                                                                                                                                                                                                            4)
                                                                                                   57;
                                                                                                                                                                                                4).
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                    53;
                                                                            ----V 28
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on
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                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                or send an email to license@isb-sib.ch).
                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                    POMAIN: The BH4 domain is required for anti-apoptotic for interaction with RAF-1 (By similarity).

If or interaction with RAF-1 (By similarity).

If SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

INTERACTY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

INTERACTY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

INTERACTY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q00709;
01-APR-1993
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
"Molecular cloning and DNA sequence analysis of cDNA encoding chicken homoloque of the Bcl-2 oncoprofein ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92379084; PubMed=1511008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93375724; PubMed=1508712; Eguchi Y., Ewert D.L., Tsujimoto Y.; "Isolation and characterization of the chicken bc1-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis regulator Bcl-2.
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nomologue of the Bcl-2 oncoprotein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCL2_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
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                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and BCl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity). SUBCELULIAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen, kidney, heart, ovary and brain, with the highest levels in the
                                                                                                                                                                                                                                                                                                              thymus. In the embryo, highly levels expressed in all tissues with high levels in the bursa of Fabricius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                         activity and
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Best Local
                                                                                                                                                                        2_BOVIN
BCL2_BOVIN
002718;
                     SEQUENCE FROM N.A.
STRAIN-HOLSTEIN; TISSUE-Thymus;
                                                                 Eukaryota; Metazoa; Chordata; Crania
Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Bovinae; Bos.
                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Apoptosis regulator Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
SEQUENCE
              Reyes R.A.,
                                                           NCBI_TaxID=9913;
                                                                                                     Bos taurus (Bovine).
Bovine leukemia virus associated-leukemogenesis is correlated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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EMBL; D11381; BAA01978.1; JOINED.
EMBL; D11961; CAA78018.1; -.
PIR; A37332; A37332.
PIR; S24390; S24390.
                                                                                                                                                                                                                                       190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK
                                                                                                                                                                                                                                                          145 AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000712; Bcl_2. Pfam; PF00452; Bcl-2; 1. Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                     130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002475; BCL2
InterPro; IPR003093; BH4.
                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                           70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129
                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                             9 DTRALVADFVGYKLRQKGYVCGAG-----PGEGPAADP------
                                                                                                                                                                                                                                                                               ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW
                                                                                                                                                                                                                                                                                                    ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                                       DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69
                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q07817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01260;
PS50063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50062; BCL2_FAMILY; 1.
PS01080; BH1; 1.
PS01258; BH2; 1.
PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002475; BCL2_family.
              Cockerell G.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
87
130
181
208
64
67
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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139
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                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
139
                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25687 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 423.5; DB 1;
Pred. No. 5.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
E -> S (IN REF. 2
GSAAASEVPPAEGLRP
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5252555ACB6E4C3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                              Ruminantia;
                                                                                                                                                                                 229
                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2).
(P -> ARLLLVRCPRLRGCA
                                                                              Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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4.

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with suppression of programmed cell death and increased expression of Bcl-2.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                  Apoptosis;
                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U92434; AAB53319.1;
HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003093;
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002475; BCL2_family.
                                                               TRANSMEN
                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle(By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphorylated by similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity). SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and BG1-X(L). Heterodimerization with BAX requires intact BH and BH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity). SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for interaction with RAF-1 (By similarity).
PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: The BH4 domain is required for anti-apoptotic activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                     SM00337; BCL; 1.
SM00265; BH4; 1.
                                                                                                                                                                                                                                                                      PS50062; BCL2
PS01080; BH1;
                                                                                                                                                                                                  PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit
                                                                                                                                                                                                                                       PS01259;
                                                                                                                                                                                                                                                                                                                                                                            IPR000712; Bcl_2.
                                                                                                                                                                                  Transmembrane; Mitochondrion; Phosphorylation
                                                            10
64
69
83
126
177
202
              AA.
                                                                                                                                                                                                                                                                                        BCL2_FAMILY; 1.
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68
72
97
145
192
223
35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     institutions as long
              MW;
                             POTENTIAL.

CLEAVAGE (BY CASPASES) (BY SIMILARITY)
PHOSPHORYLATION (BY PKC) (BY SIMILARIT
                                                                                                                                                   POLY-PRO
ADIDDOAF98FFFIID CRC64;
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY; TISSUE-Ovary;

MEDLINE=95129487; PubMed=7828536;

Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;

"Expression of members of the bcl-2 gene family in the immature rat

"expression of members of the bcl-2 gene family in the immature rat

ovary: equine chorionic gonadotropin mediated inhibition of granulosa
cell apoptosis is associated with decreased bax and constitutive
bcl-2 and bcl-xlong messenger ribonucleic acid levels.";

Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL2_RAT STANDARD; PRT; 236 AA P49950; Q62837; Q64032; Q1-0CT-1996 (Rel. 34, Created) Q1-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
MEDLINE=94193015; PubMed=8144041;
Sato T., Irie S., Krajewski S., Reed J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein."; Gene 140:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 19-172 FROM N.A. MEDLINE=95059917; PubMed=7969891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL2 OR BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis regulator Bcl-2.
                                      -
                                                                                                                                                                                                                                                  Neuroscience 61:165-177(1994).
                                                                                                                                                                                                                                                                                    "bcl-2 messenger RNA is localized adult rat brain.";
                                                                                                                                                                                                                                                                                                                             Lindholm D.;
                                                                                                                                                                                                                                                                                                                                             Castren E., Ohga Y., Berzaghi M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 ALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130
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the apoptosis-activating factor (APAF-1).
SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and BC1-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity) similarity) outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. TISSUE SPECIFICITY: Expressed in a variety of tissues, with
                                                                                                                                                                 FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFT
                                                                                                                                                   release of cytochrome c from the mitochondria and/or by binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNREIVMKYIHYKLSQRGYEWDAGDAGAAPPGAAPAPGILSSQPGRTPAPSRTSPPPPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELYG----PSMRPLFDFSWLSLKALLSLAL-VGACITLGAYLGHK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGVNWGRIVAFFEFGGVMCVESVNREMSPLVDSIALWMTEYLNRHLHTWIQDNGGWDAFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86;
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Pred. No. 2.3e-30;
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                                                                                                                                                                                                                                                                                                                                                   Thoenen H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
-i- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).
-i- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-i- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH4).
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro;
        10
                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arPro; IPR002475; BCL2_fa

arPro; IPR003093; BH4.

arPro; IPR000712; BCL_2.

n; PF00452; BCL-2; 1.

n; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal brain, expression is higher and localized in the neuroepithelium
DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).
                                                      DTRALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L14680; AAA53662.1; -. U34964; AAA77687.1; -. S74122; -; NOT_ANNOTATE Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E; PS50062; BCL2_FAMIL;
E; PS01080; BH1; 1.
E; PS01258; BH2; 1.
E; PS01259; BH3; 1.
E; PS01260; BH4_1; 1.
E; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00337; BCL;
SM00265; BH4;
                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the cortical plate.
                                                                                                           Conservative
                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL2_FAMILY;
                                                                                                                                                                                                                                                                                             30
104
152
199
230
35
70
70
42
157
                                                                                                                              41.1%;
36.2%;
                                                                                                                                                                                                                                            26622 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCL2_family.
                                                                                                                                                                                                                                                    BH2.

POTENTIAL.

CLEAVAGE (BY CASPASES) (BY SIMILARITY).

PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

A -> R (IN REF. 2).

E -> G (IN REF. 2).

S -> Y (IN REF. 2).

L -> Q (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion; Phosphorylation
                                                                                                        34;
                                                                                                                                 Score 414; DB 1
Pred. No. 4e-30;
                                                                                                                                                                                                                                         E7688CB9071A872A CRC64;
                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                            <u>ب</u>
                                                                                                           62;
                                                                                                                                                      Length 236;
                                                                                                     Indels
                                                                                                     52;
                                                                                                  Gaps
                                                                                                     ω
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RESULT
BCL2_MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
        + +
                                                                                                                                                                                                                                                                                                           Deng X., Ito T., Carr B., Numby M., May W.S. Jr.;
"Reversible phosphorylation of Bcl2 following interl
bryostatin 1 is mediated by direct interaction with
phosphatase 2A*.";
                                                        <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97277291; PubMed=9115213; Ito T., Deng X., Carr B., May W.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P10417; P10418;
01-MAR-1989 (Rel. 10, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BALB/C; TISSUE-Liver; MEDLINE-87187643; PubMed-3032455;
                                                                                                                                                                                                                                                                                                                                                                                                    DEPHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                  "Bcl-2 phosphorylation required for anti-apoptosis function.
J. Biol. Chem. 272:11671-11673(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92375724; PubMe
Eguchi Y., Ewert D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO 221-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.; "Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma."; Cell 49:455-463(1987).
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99069407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION BY PKC, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Isolation and characterization of the chicken bcl-2 gene: expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL2 OR BCL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis regulator Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                               the apoptosis-activating factor (APAF-1).
SUBUNIT: Forms homodimers, and heterodimers with BAX, Bcl-x(L). Heterodimerization with BAX requires intact domains, and is necessary for anti-apoptotic activity similarity). Also interacts with APAF-1 and RAF-1.
SUBCELLULAR LOCATION: Outer mitochondrial membrane, ir membrane of the nuclear envelope and the endoplasmic ranged by alternatic scaling alpha (shown here) are produced by alternatic scaling.
                     are produced by alternative splicing. TISSUE SPECIFICITY: Expressed in a va
                                                                                                                                                                                        permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding
                                                                                                                                                                                                                                      FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cell Regulates cell death by controlling the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variety of tissues including lymphoid t and embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                               Chem.
                                                                                                                                                                                                                                                                                               273:34157-34163(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=1508712;
D.L., Tsujimoto Y.;
                                                                                                                                                                                                                                                                                                                                                                                  PubMed=9852076;
     Expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGENESIS
   required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND BETA)
                                                                                                                                                                                                                                                                                                                                           May W.S. Jr.; following interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236
variety of tissues. for anti-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      읁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuronal organs
                                                     here) and
                                                                                                                                                                                                                                                                                                                             protein
                                                                                      intracellular
                                                                                                                                                                                        by binding to
                                                                     reticulum
                                                                                                                     BAD,
BH1 (
     activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193
                                                                                                                                                                                                                                                                                                                                                 ç
                                                       beta;
                                                                                                                                        and
                                                                                                                                                                                                                                                             cells.
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                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                            SMARY; SM0033; BCL; 1.
SMARY; SM0035; BH4; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS011258; BH2; 1.
PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                         SEQUENCE
                                                                                                                                                           VARSPLIC
                                                                                                                                                                  Phosphorylation.
DOMAIN 10
DOMAIN 90
DOMAIN 133
DOMAIN 134
TRANSMEM 209
SITE 34
MOD_RES 70
TRANSMEM 70
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                     Apoptosis;
                                                                                                                                                                                                                                                                                                                                           Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1
                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
InterPro; IPR000712; Bcl_2.
70 SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                               10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                Local
                                                            9 DTRALVADFVGYKLRQKGYYCGAG------PG-----PG-----
                  -----EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                        DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART 69
                                                                                                                                                                                                                                                                                                                                                                                               ; Q07817; 1MAZ.
MGI:88138; BC12.
                                                                                                                                                                                                                                                                                                                                                                                                                  B25960; TVMSB1.
E37332; E37332.
                                                                                                                                                                                                                                                                                                                                                                                                                                         A25960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 M16506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for interaction with RAF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L31532;
                                                                                               Similarity
                                                                                                                                                                                                                                                            PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                   Alternative
                                                                                                                                        236 AA;
                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         TVMSA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA37282.1; -.
AAA37282.1; JOINED.
AAA37281.1; -.
                                                                                                                                                          30
104
152
199
230
230
70
236
                                                                                            41.0%;
                                                                                                                                      26425
                                                                                                                                                                                                                                               splicing; Transmembrane; Mitochondrion;
                                                                                                                                     WW;
                                                                                 34; Mismatches
                                                                                             Score 413; DB 1;
Pred. No. 4.9e-30;
                                                                                                                                   POTENTIAL.

CLEAVAGE (BY CASPASES) (BY SIMILARITY).

PHOSPHORYLATION (BY PKC).

DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL

GHK -> VGACLIVE (IN ISOFORM BETA).
                                                                                                     Length 236;
                                                                                 Indels
                                                                                 52;
                                                                                Gaps
                                                                               5
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A COCO SON SERVICE SER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
         apoptosis
                  Yin X.-M., Oltvai Z.N., Korsmeyer S.J., "BHI and BH2 domains of BCl-2 are required for inhibition of
                                                                                       MEDLINE=94239528;
                                                                                                                                                                                                                                                                                                                                                                                                   oncogenes of non-Hodgkin's lymphomas.";
                                                                                                                                                                                                                                                                                                                                                                                                                     Tanaka S., Louie D.C., Kant J.A., Reed J.C.; Frequent incidence of somatic mutations in translocated BCL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-Ig fusion gene in lymphoma.";
                                                                                                                                                                                                    "Bcl-2 is an inner mitochondrial membrane protein that blocks programmed cell death.";
                                                                                                                                                                                                                                                                 Hockenbery D.,
                                                                                                                                                                                                                                                                                   MEDLINE=91066924; PubMed=2250705;
                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92096610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S., Goldman P., Korsmeyer S.J.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cleary M.L., Smith S.D., Sklar J.;
"Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobul," transcript resulting from the t(14,18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-131 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88196071; PubMed=2834197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translocation.";
Cell 47:19-28(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM ALPHA MEDLINE=87002488; PubMed=2875799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eguchi Y., Ewert D.L., Tsujimoto Y., "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS TO 96; 110 AND 237.
MEDLINE=92375724; PubMed=1508712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsujimoto Y., Croce C.M.;
"Analysis of the structure, transcripts, and protein products "Analysis of the involved in human follicular lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA) MEDLINE=86259760; PubMed-3523487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                           79:229-237(1992).
                                                                                                                                                                      mmed cell death.";
348:334-336(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7:123-131(1988)
         and
heterodimerization with Bax.";
                                                                                                                                                                                                                                                              Nunez G.,
                                                                                    PubMed=8183370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=1339299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORM ALPHA).
                                                                                                                                                                                                                                                           Milliman C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISOFORM ALPHA), AND VARIANTS NHL
                                                                                                                                                                                                                                               Schreiber R.D., Korsmeyer S.J.;
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"BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal protein kinase pathway normally activated at G(2)/M.";
Mol. Cell. Biol. 19:8469-8478/1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98057466; PubMed=9395403;
Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLEAVAGE BY CASPASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruvolo P.P., Deng X., May W.S.;
"phosphorylation of Bc12 and regulation of apoptosis.";
Leukemia 15:515-522(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 369:321-323(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21260650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20036804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVIEW ON PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION BY ASK1/JNK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
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modified and this statement is not removed. Usage by an
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                                      EMBL;
                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                EMBL;
                                                                                EMBL; M13994;
                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAP-1. SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; ALTERNATIVE PRODUCTS: 1 isoforms; alpha (shown here) and beta;
                                                                                                                                                                                                                                                                                                                                                                                                                         Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).

PPM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic. activity, causes the release of cytochrome c into the cytosol artivity, causes the release of cytochrome c into the cytosol promoting further caspase activity.

DISBASE: Involved in follicular lymphoma (FL) (also known as type II chronic lymphatic leukemia) by a chromosomal translocation t(14;18)(q32;q31) which involves Bcl2 and immunoglobulin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in a variety of tissues.
DOMAIN: The BH4 domain is required for anti-apoptotic activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the
                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pTM: phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       release of cytochrome c from the mitochondria and/or by binding to the apoptosis activating factor (APAF-1).
                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE BCL-2 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                regions
M13995;
M14745;
X06487;
S72602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278:1966-1988(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interaction with RAF-1.
  AAA51814.1; ALT_SEQ.; AAA35591.1; -.; CAA29778.1; -.; AAD14111.1; ALT_SEQ.
                                                                                      AAA51813.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=10567572;
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Best Local S
Matches 87
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PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; D37332; D37332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR;
                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1
SMART; SM00265; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; Q07817
MIM; 151430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000712; Ffam; PF00452; Bc1-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proto-oncogene: Apoptosis; Alternative splicing; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polymorphism;
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                                                                                                                                                                                                                                                                                                                                          MUTAGEN
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                                                                                                                                                                                                                                                                                               MUTAGEN
                                                                                                                                                                                                                                                                                                                   MUTAGEN
                                                                                                                                                                                                                                                                                                                               MUTAGEN
190 QDNGGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
                    139 HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                10 DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART 69
                                                                 79
                                                                                    70 SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR 129
                                                                                                            36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; B29409; TVHUB1.
; A24428; TVHUBC.
; C37332; C37332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A29409; TVHUA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q07817; 1MAZ
                                                                                                                                                      DTRALVADEVGYKLRQKGYVCGAG-------PGE-----PGE------
                                           FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWI 138
                                                                                                                                                                          al Similarity
87; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01259;
PS01260;
PS50063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50062; BCL2_FAMILY;
PS01080; BH1; 1.
PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002475;
                                                                                                                                                                                                                                 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187
212
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                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          59
                                                                                                                                                                                                                                                                                                                               34
64
                                                                                                                                                                                                                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation; Chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH4_2;
                                                                                                           -GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR 78
                                                                                                                                                                                                                                           48
59
117
129
                                                                                                                                                                                                                                                                                                188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155
                                                                                                                                                                                                                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bc1_2.
                                                                                                                                                                                     41.0%;
37.0%;
                                                                                                                                                                                                                                  26266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCL2_family.
                                                                                                                                                                              34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           /FTId=VAR-V
                                                                                                                                                                                                                                           LOSS OF ANTI-APOPTOTIC ACTIVITY.

1 -> F (IN REF. 4).

P -> T (IN REF. 3).

S -> R (IN REF. 3).

R -> C (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.

CLEAVAGE (BY CASPASE-3).

PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

DAFVELYGPSMRPLFDESMLSLKTLLSLALVGACITLGAYL
                                                                                                                                                                                        Score 412.5;
Pred. No. 5.5
                                                                                                                                                                                                                                                                                                LOSS OF ANTI-APOPTOTIC ACTIVITY. W->A: NO HETERODIMERIZATION WITH BAX AND
                                                                                                                                                                                                                                                                                                                                                                 MUTATION)
                                                                                                                                                                                                                                                                                                                                                                                                 MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR_000827
                                                                                                                                                                                                                                                                                                                                                     /FTId=VAR_000829
                                                                                                                                                                                                                                   3C49F2B714DC9CCB
                                                                                                                                                                                                                                                                                                                                                                           I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                ABOLISHES CLEAVAGE BY CASPASE-3
NO EFFECT ON CLEAVAGE BY CASPASI
                                                                                                                                                                                                                                                                                                                      NO HETERODIMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                         (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                          VGASGDVS (IN ISOFORM BETA)
                                                                                                                                                                                           .5e-30;
                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                    Length 239;
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                   BY CASPASE-3
                                                                                                                                                                                                                                                                                                                          WITH BAX AND
                                                                                                                                                                                 55;
                                                                                                                                                                                 Gaps
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BCL2_CRILO
Q9JJV8;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20431763; PubMed=10973819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10030;
                                                                                                                                                                                                                                                                                                                                      cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytos promoting further caspase activity.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES. MEDLINE=21092839; PubMed=11181062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomicic M.T., Christmann M., Kaina B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          romicic M.T., Kaina B.;
rhamster Bc1-2 protein is cleaved in vitro and in cells by caspase-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 275:899-903(2000)
                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding the apoptosis-activating factor (APAF-1) (By similarity). SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).

PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and conser-70 by PKC is required for the anti-apoptosis activity and the serior of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hem. Biophys. Res. Commun. 281:404-408(2001). FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bcl-x(L), Heterodimerization with BAX requires intact BH1 and BH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: Proteolytically cleaved by caspases during apoptosis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity). Dephosphorylated by protein phosphatase
   AJ271720; CAB92245.1;
P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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    A LOCAL COLOR RESERVED TO THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR11_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00452; Bc1-2;
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1
SMART; SM00265; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AR11_XENLA
Q91828;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50062; PROSITE; PS01080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002475;
InterPro; IPR003093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
Apoptosis regulator R11 (XR11)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                  Cruz-Reyes J., Tata J.R.;
                                                                                                                                                                                                                                                            MEDLINE=95331613; PubMed=7607538;
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                                                                                                              "Cloning,
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 -----VCGAGPGEGPAADPLHQAMRAAGDEFETRERRTESDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 DTRALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGWDAFVELYG----PSVRPLFDFSWLSLKTLLSLAL-VGACITLGTYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS
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                                                                                                                                                                                                            characterization and expression of two Xenopus bcl-2-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                            Xenopus.
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BH4_2; 1.
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BH2;
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104
152
199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH2.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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Search completed: June 10, 2002, 10:32:13 Job time: 346 sec
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                                                                                                                                                                                                                                                                                                                                                                            Query Match 36.8
Best Local Similarity 42.1
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X82461; CAA57844.1; -. HSSP; Q07817; IMAZ.
                                                                     184 RLLTI-VMLTGVFAL 197
                                                                                                 166 NWASVRTVLTGAVAL 180
                                                                                                                        124 VESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFG 183
                                                                                                                                          108 AESVNKEMEPLVGQVQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--G 165
                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                64 EATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRDGTNWGRIVAFFSFGRALC 123
                                                                                                                                                                                                                                                                  48 AAGDEFETRERRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALC 107
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                                                                                                                                                                                                                                       SRDLVEKFVSKKLSQ-NEACRKFSNNPNPMPYLMEPSTSERPGEGATQGIVEEEVLQALL 63
                                                                                                                                                                                                                                                                                                                                                                   101 120 BH1.
152 167 BH2.
181 198 POTENTIAL,
204 AA; 23379 MW; 3BFC6BE6DDA4CA03 CRC64;
                                                                                                                                                                                                                                                                                             36.8%; Score 371; DB 1; Length 204;
42.1%; Pred. No. 2.4e-26;
ative 25; Mismatches 62; Indels 26; Gaps
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                        SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_manmal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_phage:*
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sp_bacteria:*
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                                                              sp_vertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score 996	Query Match	Query Query Match Length DB	DB	ID 088996
ω	440.5	43.7	233	σ	Q9MYW4
4	435.5	43.2	233	11	035844
ъ	431.5	42.9	233	σ	Q9N1A2
6	428.5	42.6	233	σ	Q9MZS7
7	403	40.0	238	13	090Z98
8	401	39.8	180	σ	Q9BDD5
9	401	39.8	217	11	Q99N35
10	399	39.6	236	11	Q923R6
11	398.5	39.6	180	σ	Q9BDX7
12	374.5	37.2	188	11	Q9QWX2
13	374.5	37.2	235	11	035843
14	373.5	37.1	188	4	Q9H1R6
15	373	37.0	204	13	Q90ZH2
16	347	34.5	219	11	Q99N36

Query Match

98.98;

Score 996;

DB 11;

Length 193;

23 159.5 24 159.5 25 1148.5 26 148.5 27 146.5 28 144.5 29 143.3 30 142.5 31 141.3 31 131.5 32 133.5 34 135.5 35 131.5 36 131.5 37 130.5 38 130.5 39 130.5	17 189 18 185 19 176.5 20 171.5 21 168.5 22 163
116.1 116.1 117.2 114.3 114.3 114.3 114.3 114.3 113.4 113.4 113.3	18.8 18.4 17.5 17.0 16.7
235 173 173 179 149 149 177 177 177 215 211 211 211 213 213 213 213 213 213 330 330 331	209 170 192 221 125
4 11113 113 113 113 113 113 113 113 113	
Q967D2 Q9M256 Q9M754 Q9M754 Q9M754 Q9M777 Q9CM67 Q9CM7 Q9DZN1 Q9EF7 Q9DZN1 Q9M6F1 Q9M6F1 Q9M8F1 Q9M8F1 Q9M8F1 Q9M8F1 Q9M8F1 Q9M8F3	Q9JK59 Q9WUI5 Q9I9N4 Q98U13 Q9H1R5 Q9R1B3
O967d2 geodia cydo O9m256 ovis aries O991x13 rattus norv O9m754 suberites d O9m977 homo sapien O9gm97 ovis aries O90zm1 gallus gall O9e1f2 meleagrid h O919m3 brachydanio O9w6f1 gallus gall O9m76 homo sapien O9umx3 homo sapien O9umx3 homo sapien O91812 rattus norv O9dh00 meleagrid h O91132 homo sapien O91812 gallus gall O90f5 gallus gall O90f6 peromyscus O93w6 peromyscus	Q9jk59 rattus norv Q9wui5 rattus norv Q9i9n4 brachydanio Q9Bul3 xenopus lae Q9hlr5 homo sapien Q9rlb3 rattus norv

ALIGNMENTS

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RESULT 1
088996
088996
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
DT 01-DCC-2001 (TrEMBLrel. 19, Last annotation update)
DE BCL-W.
GN BCL-W.
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; RRI [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAMLEY; TISSUE=BRAIN;
RX MEDLINE=99292146; PUMPMed=10366024;
RA Hamner S. Skoglosa Y. Lindholm D.;
Toliferential expression of bcl-w and bcl-x messenger RNA in the developing and adult rat nervous system.";
RR Neuroscience 91:673-684(1999).
DR EMBL; ARO96291; AAC64200.1; -.
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR002475; BCL2_family.
DR InterPro; IPR003093; BH4_1.
DR Pfam; PF001452; BCl-2; 1.
DR Pfam; PF001452; BCl-2; 1.
DR PFAM; SM00337; BCL; 1.
DR SMARR; SM0035; BCL-2; 1.
DR PROSITE; PS01060; BH1; 1.
DR PROSITE; PS01060; BH2; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01258; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS01260; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS01260; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS01260; BH3; 1.
DR PROSITE; PS01260; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS01260; BH3; 1.
DR PROSITE; PS01260; BH3; 1.
DR PROSITE; PS01260; BH3; 1.
DR PS0160; BH3; 1.
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Best Local Similarity

98.4%;

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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Kurotone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Park H., Weitz C., Wanati H., Kohtenki S.
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01-JUN-2001 (TrEMBLrel. 17, Cr
01-JUN-2001 (TrEMBLrel. 17, La
01-DEC-2001 (TrEMBLrel. 19, La
BCL2-LIKE 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
PROSITE: PS50062; BCL2_FAMILY; 1.
PROSITE: PS01080; BH1; 1.
PROSITE: PS50063; BH4_2; 1.
SEQUENCE 178 AA; 19147 MW; E2
                                                                        Pfam; PF00452; Bcl-2; 1. Pfam; PF02180; BH4; 1. SMART; SM00337; BCL; 1. SMART; SM00265; BH4; 1.
                                                                                                                                              InterPro: IPR002475; BCL2_family.
InterPro: IPR000712; Bcl_2.
InterPro: IPR003093; BH4.
                                                                                                                                                                                                                                              EMBL; AK013244;
                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=EMBRYO; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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                                                                                                                                                                                                         MGI:108052; Bc1212.
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                                                                                                                                                                                                                            Q07817;
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Last annotation update)
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1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; | Sciurognathi; Muridae;
   E2D4C3F79528E9D7 CRC64;
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Best Local :
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PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL; AY005131; AAF88137.1; ... HSSP; P53563; IAF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50062; BCL2_FAMILY; 1. PROSITE; PS01080; BH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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186
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GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                      GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                   VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMEVLVSRIAAWMATYLNDHLEPWIQEN
                                                                                                                            VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                                                       RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTGPEMETPSAINGNPAWHPADSPAV 65
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PF02180; BH4; 1.
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SM00265; BH4;
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PS50063;
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PS01259;
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BH4_2;
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вн3;
                                                                                                                                                                                                                  -----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                       43.7%;
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H4_2; 1.
25986 MW;
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95.3%;
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                                                                                                                                                                                                                                                                                                                                               22;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                     Score 440.5;
Pred. No. 3.
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              12F0F30344D53F93 CRC64;
                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2e-59;
                                                                                                                                                                                                                                                                                                                                                                       .5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus
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                                                                                                                                                                                                                                                                                                      -----PGEGPAA. 39
                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 178;
                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                              233;
                                                                                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                      185
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RESULT
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Q9N1A2
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Best Local
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE-98051053; PubMed-9390687; Yang X.-F., Weber G.F., Cantor H.; "A novel Bcl-x isoform connected to apoptosis in T cells."; Immunity 7:629-639(1997).
EMBL: U51278: AAC53459.1; -.
EMSP: P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PROSITE; PS50062; BCL2_FAMILY; 1
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                035844;
035844;
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
PROSITE;
PROSITE;
SEQUENCE
                                            Q9N1A2 PRELIMINARY; PRT; 233 AA.
Q9N1A2;
Q9N1A2;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation updata ANTI-APOPTOTIC REGULATOR BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
 Mammalia;
           Eukaryota;
                       Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCL2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                       141
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                                                                                                                                                                                                                         QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                              RALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:88139; Bc121
                                                                                                                                                                                       SGGWAEFTALYGDGALEEARRLREG--NWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                           NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                   CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                NGGWDTFVDLYGNNAAAESRKGKEGFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                               QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                          RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65
                                                                                                                                                                                                                                                                                                                                                      94;
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
233 AA; 26033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01259;
PS01260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002475; BCL2_family. IPR000712; Bcl_2. IPR003093; BH4.
 ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=THYMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                  43.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05,
19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                  Score 435.5;
Pred. No. 9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                               3083F2D8327E072E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                   .6e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell receptor regulates
                                                                                                                                                                                                                                                                                                                                                                             DB 11;
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                                                        update)
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                                                                                                                                                                  229
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 Euteleostomi; Sus.
                                                                                                                                                                                                                                                                                                                                                                              233;
                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus
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DETERMINATION OF THE PROPERTY 
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Best Local
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09MZS7:
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2001 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL-X LONG PROTEIN.

Ovis aries (Sheep).

Ovis aries (Sheep).

Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;

Bunmalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea

Bovidae; Caprinae; Ovis.

NCBI_TaxID=9940;

[1]
InterPro; IPR002475; BCL2_family InterPro; IPR000712; Bcl_2. InterPro; IPR003093; BH4. Pfam; PF00452; Bcl-2; 1. Pfam; PF00452; Bcl-2; 1. SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                        Murray J.F., Dong Y.B., Leigh A.J., "Bcl-x in the sheep ovary."; submitted (JUL-1999) to the EMBL/Ger EMBL; AF164517; AAF89532.1; -. HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00452; Bc1-2; 1
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM TISSUE=HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
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InterPro; IPR000712; Bcl_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee T.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAXLETRLADWIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE
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PS01080; BH1; 1.

PS01258; BH2; 1.

PS01259; BH3; 1.

PS01259; BH3; 1.

PS01260; BH4_1; 1.

PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 42.9%;
Similarity 41.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 2.2e-30;
1; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2FA312818B25E17D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Scaramuzzi R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                        Carter N.
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Best Local Similarity
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Best Local
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01-DEC-2001
01-DEC-2001
01-DEC-2001
BCL-XL-LIKE
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PROSITE;
PROSITE;
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PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (2ebrafish) (2ebra dar
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii, neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                    zebrafish, Danio rerio(1).";
Biochim. Biophys. Acta 1519:127-133(2001).
EMBL; AF317837; AAK81706.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            BLP1
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=21299061; PubMed=11406282;
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                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                      "Cloning
                                                                                                                                                                                                                                                                                    Chen M.-C.,
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
139
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                                                                                                                                 11 RALVADFVGYKLRQKGYVC--
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HSSGGWAEFTALYGDGALEEARRLREG - - NWA - SVRTVLTGAVALGALVTVGAFFASK
                                      FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWNVAYLETRLADWI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQEN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS
                       FESVMDEVFRDGVNWGRIVGLFAFGGALCVECVEKEMSPLVGRIAEWMTVYLDNHIQPWI
                                                                   GTPPQSPASSPQRQTNGSGGLDAVKEALRDSANEFELRYSRAFNDLSSQLHITPATAYQS 125
                                                                                            --PGEGPAADPLHQ----
                                                                                                                  RELVVFFIKYKLSQRNYPCNHIGLTEDTNRTDGAEENGEGAAGATTLVNGTMNRTNASST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTE; PS01026; BH4; 1.
TTE; PS01062; BCL2; FAMILY; PS01080; BH1; 1.
TTE; PS01258; BH2; 1.
TTE; PS01259; BH3; 1.
TTE; PS01259; BH4; 1.
TTE; PS01260; BH4_1; 1.
TTE; PS01063; BH4_2; 1.
SNCE 233 AA; 26134 MW;
                                                                                                                                                                 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                      C., Gong H.-Y., Cheng C., Wang J.-P., Hong
and characterization of zfBLP1, a Bcl-XL
                                                                                                                                                                                                                           238
                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 19, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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BCL2_FAMILY;
                                                                                                                                                                                                                           26253 MW;
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                                                                                                                                                                            40.0%;
36.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                 19,
                                                                                  ----AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR
                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                               Score 403; DB Pred. No. 7.3e 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 428.5; DB Pred. No. 4e-30;
                                                                                                                                                                                                                                                                                                                                                   (Zebra danio).
Craniata; Vertebrata; I
Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                           6E58394933EEFDDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                238
                                                                                                                                                               DB 13;
7.3e-28;
hes 62;
                                                                                                                                        -GAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
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                                                                                                                                                                                                                                                                                    Hong
                                                                                                                                                                                                                           CRC64;
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                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                        g J., Wu J
homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
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                                                                                                                                                                62;
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193
                                                                                                                                                                Gaps
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10 BDD5
10 BDD5
10 BDD5
20 BD7
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Q99N35
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Best Local s
Matches 76
STRAIN-129/SVJ;
Yang X.-F., Cant
"Novel cDNA stru
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NON_TER
SEQUENCE
                                                                                                              BCLX.
Mus musculus (Mouse).
Mus musculus (Mouse).
harvota; Metazoa; Chordata;
harvota; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9BDD5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
                                                                                                                                                                                                                       01-JUN-2001 (TrembLrel. 17, 01-JUN-2001 (TrembLrel. 17, 01-DEC-2001.(TrembLrel. 19, B-CELL LEUKEMIA/LYMPHOMA X (
                                                                                                                                                                                                                                                                                              Q99N35;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2000) to the EMBL; AF245488; AAK31307.1; EMBL; AF245489; AAK31308.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; BCL2.
Pfam; PF00652; BCL2; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos. NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                          Q99N35
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                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of the bovine bcl-xL gene and related Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 QAMRAAGDEFETRERRTFSDLAAQLHVTPGSAQQRETQVSDELFQGGPNWGRLVAFFVFG 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERFNRWFLTGMTVAGVVLLGSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E--GNWASVRTVLTGAVALGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q07817; 1MAZ
  cDNA structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50062; BCL2_FAMILY; PS01080; BH1; 1. PS01258; BH2; 1.
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180 AA;
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                       Η.;
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  genomic
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                                                                                                                                                                                                                            (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183
                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 401; DB 6;
Pred. No. 7.7e-28;
9; Mismatches 4!
                                                                                                                              Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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  organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                             217
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                                                                                                                                                        Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --
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                                                                                                                                        Muridae;
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  of.
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  apoptosis regulatory
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                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
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                                                                                                                                        Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pseudogenes.";
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RESULT
Q923R6
ID Q923R6
ID Q923R6
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Best Local
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01-DEC-2001
01-DEC-2001
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF133282; AAK15455.1; -..
EMBL; AF133281; AAK15455.1; JOINED.
HSSP; P53563; IAF3.
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PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lai D.Z., Chen W., Wang H.T.; Construction of a robust CHO cell line for biopharmaceutical "Construction of a robust CHO cell line for biopharmaceutical submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF404339; AAK92201.1: -
SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8BB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B-CELL LYMPHOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q923R6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 AALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 E--GNWASVRTVLTGAVALGAL 183
  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 QAMRAAGDEFETRERRTESDLAAQLHVTPGSAQQRETQVSDELEQGGPNWGRLVAFEVFG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG
                                                       82
                                                                                                              70
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                                                                                                                                                                                                                       DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART
                                                                                                                                                                                                                                                                               DTRALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERFNRWFLTGMTVAGVVLLGSL 213
  VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN
                                                    VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                           SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                                                                                                                                                \hbox{\tt -----} VCGAGPGEGPAADPLHQAMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQRFTQ
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76; Conserv
                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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35.3%;
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                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                   Score 399; DB 11;
Pred. No. 1.6e-27;
32; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 401; DB 11;
Pred. No. 9.7e-28;
9; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3B5A4E809A7DEF18 CRC64;
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                                                                                                                                                                                                                                                                                                                                         66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 217;
                                                                                                                                                                                                                                                                                                                                                                                       Length 236;
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                                                                                                                                                                                                                                                                                                                                         52;
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     189
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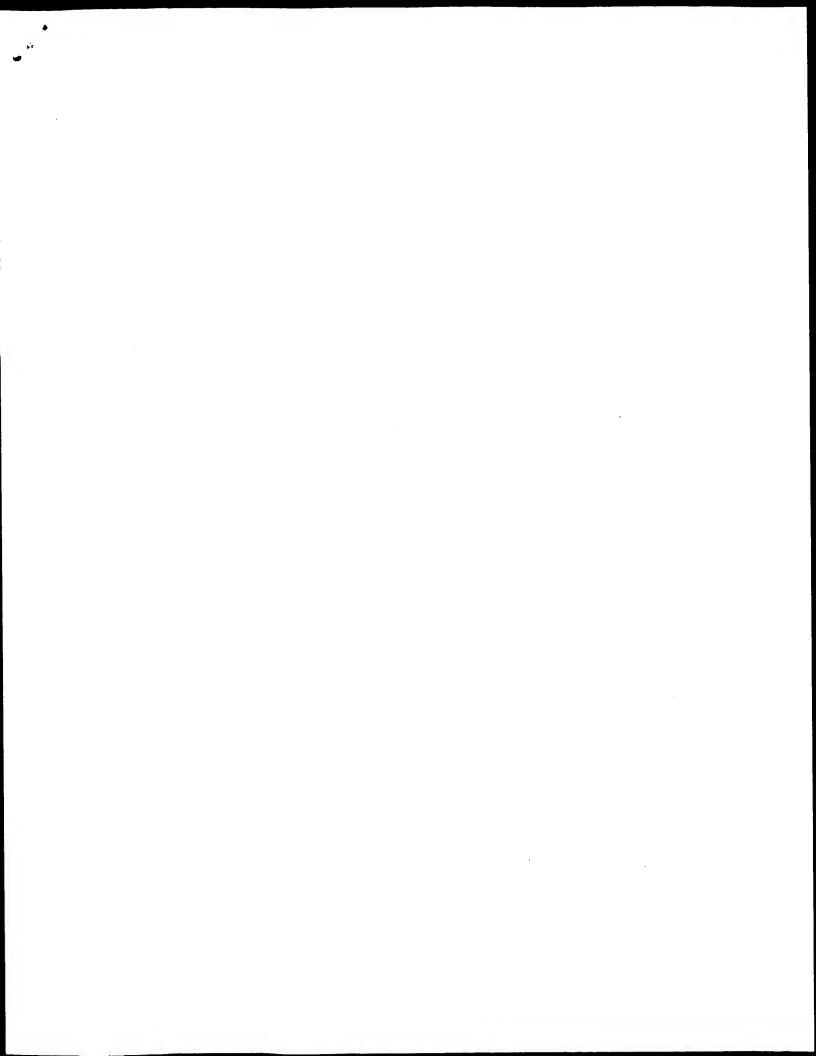
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RESULT
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Best Local :
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NON_TER
SEQUENCE
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PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002475; BCL2_family
IPR000712; BCL_2.
Pfam; PF00452; BCL-2; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the EMBL; AF245487; AAK31306.1; HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BDX7
                                                                                                                                                                                                                         Q9QWX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Amills M., Bouzat J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9BDX7
MEDLINE=20350651; PubMed=10894153;
Rucker E.B. III, Dierisseau P., Wagner K.U., Garrett L.,
Wynshaw-Boris A., Flaws J.A., Hennighausen L.;
"Bcl-x and Bax regulate mouse primordial germ cell survi
                                                                                                                                                                  01-MAY-2000 (TREMBLIEL. 13, 01-MAY-2000 (TREMBLIEL. 13, 01-DEC-2001 (TREMBLIEL. 19,
                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                     BCL-X (FRAGMENT).
                                                                                                                                                                                                             Q9QWX2;
                                                      SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=10090;
                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of the bovine bcl-xL gene and related pseudogenes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 GGWDAFVELYG----PSVRPLFDFSWLSLXTLLNLAL-VGACITLGTYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                126
                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                      66
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                                                                                                                                                                                                                                                                                                                                                                                                                                      20 YKLROKGYVCGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           PGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLE 131
                                                                                                                                                                                                                                                                                                DHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                          TRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                             WHLEDSPAVNGA-PGHSRSSDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHIT 65
                                                                                                                                                                                                                                                                                                                                                     {\tt PGTAYQSFEQVVNELFRDGVNWGRIVASFSFGGALCVESVDKEMQVLVSRIATWMATYLN}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50062; BCL2_FAMILY; PS01258; BH2; 1.
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180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.6%;
47.1%;
                                                                                                 Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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                                                                                                                                                                   Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 398.5; DB 6; Pred. No. 1.3e-27;
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primordial germ cell survival
                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62C4C0BD0555A9EF CRC64;
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RESULT
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Best Local Similarity
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                                                                                                                                                                                MEDLINE-98051053; PubMed-9390687; Yang X.-F., Weber G.F., Cantor H.;
"A novel Bc1-x isoform connected to apoptosis in T cells.";
Immunity 7:629-639(1997).
EMBL; U51277; AACG3458.1; -.
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O35843;
O35843;
O1-JAN-1998
O1-JAN-1998
O1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PROSITE; PS50062; BCL2_FA
PROSITE; PS01080; BH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                             Pfam; PF00452;
Pfam; PF02180;
                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                  STRAIN=B6/CBA;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCL2L.
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                                                                                             InterPro;
                                                                                                                                          InterPro;
                                                                                                                                                             MGD; MGI:88139; Bcl21.
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50062; BCL2_FAMILY; PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS01260; BH4_2; 1.
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InterPro; IPR000712; Bcl_2.
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MGD; MGI:88139; BC121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis during embryogenesis.";
Mol. Endocrinol. 14:1038-1052(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003093; BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141
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  SM00337;
SM00265;
                                                                                        IPR002475; BCL2_family.
IPR000712; Bcl_2.
IPR003093; BH4.
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                             Bcl-2; 1.
BH4; 1.
                                                                                                                                                                                                                                                                                                                                                  TISSUE=THYMUS
  BCL;
BH4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.2%; Score 374.5; 42.9%; Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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hes 38;
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Best Local S
Matches 79
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Best Local
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                                                                                                                                                                      InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
InterPro; IPR000712; Bcl_2.
InterPro; IPR003093; BH4.
Pfam; PF00452; Bcl-2; 1.
Pfam; PF00180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS50063; BCL2_FAMILY; 1.
PROSITE; PS50063; BH4_2; 1.
PROSITE; PS50063; BH4_2; 1.
PROSITE; PS50063; BH4_2; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BA243J16.1.1 (BCL2-LIKE 1 (ISOFORM 1)) (FRAGMENT).
BCL2L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9H1R6;
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HSSP; Q07817; 1LXL
                                                                                                                                                                                                                                                                                                                                              Brown
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2001) to the
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                       11 RALVADFVGYKLRQKGY-----
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CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                               RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
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79; Conser
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; PS61080; BH1; 1.
; PS61259; BH3; 1.
; PS61260; BH4_1; 1.
; PS61260; BH4_2; 1.
; PS50063; BH4_2; 1.
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                                                                                                                                                             188 AA;
                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                      CAC10003.1;
                                                                                                                                                          21029 MW; 7074B6095145C324 CRC64;
                                                                                              37.1%; Score 373.5; DB 4 42.9%; Pred. No. 2.2e-25; Live 16; Mismatches 38
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42.9%;
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Pred. No. 2.
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                                                                                                                     DB 4;
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                                                                          Length 188;
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Search completed: June 10, 2002, 10:31:19 Job time: 392 sec
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                        Nakajima K., Yaoita Y.;
"Muscle cell death occurs in the regressing tail of tadpole by suicide mechanism.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055494; BAB62748.1;
EMBL; AB055494; BAB62748.1;
SEQUENCE 204 AA; 23189 MW; 1BEF1B904E29D84A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q90ZH2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BCL-XL.
BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                            10 TRALVADEVGYKLRQ------KGYVCGAGPGEGP----AADPLHQAMRA 48
                                                                                                                                                                                                                                   5 SRDLVEKFVSKKLSQNEACRKFSNNPQPNAISNGTSTSERPGEGATQGIVEEEVLQALLE 64
                                                                                            WASVRTVLTGAVAL 180
                                                                                                                                          ESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GN 166
                                                                                                                                                                             AGDEFETRERTIFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCA 108
                                                                                                                         ESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFGR 184
                                                                                                                                                                                                                                                                                        37.0%; Score 373; DB 13; Length 204; ilarity 42.8%; Pred. No. 2.7e-25; Conservative 24; Mismatches 63; Indels 2.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: /SIDS1/gcgdata/l
2: /SIDS1/gcgdata/l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  June 10, 2002, 10:25:47; Search time 55.16 Seconds (without alignments) 388.637 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-155-327E-9
1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT: *
2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT: *
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT: *
3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT: *
4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT: *
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1994.DAT: *
5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT: *
7: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT: *
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
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0: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1990.DAT: *
0: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1900.DAT: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
                                                                                                                                                                                                                                                                                                                                                                               /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1 2 3 3 4 4 4 5 6 6 7 7 10 11	Result No.
1006 1002 1002 997 997 992 992 990 990 987 970.5	Score
99.3 99.3 99.3 98.8 98.3 98.3 98.1 97.8	Query
193 193 193 193 193 193 193 193 193 193	% Query Match Length DB
20 20 20 20 20 19 20 18 20 20 20	:
AAY05531 AAW61391 AAW97391 AAW97393 AAY05530 AAW61392 AAW97392 AAW97392 AAW97392 AAW97392 AAW97392 AAW97392	ID
Mouse Bcl-w protein Rat bcl-y protein. The rat bcl-y protein. The rat bcl-y protein sequence of Human bcl-w protein Human bcl-y protein Human bcl-w protein Human bcl-w protein Human bcl-w protein Mammalian bcl-y protein Mouse Bcl-w protein Mouse Mcl-w protein Mouse Mcl-w protein Mouse Mcl-w protein Mouse Mcl-w protein	Description

Apoptosis-blocking	AAW01019	17	232	40.0	404	45
Fu-Bci-xr apoptos	AAU00222	22	485	40.3		44
Human bcl2 proto-c	AAY21120	19	272	40.3		43
BCT-2	AAB50537	22	239			42
BCL-2	AAB48288	22	239		406.5	41
ipna.	AAB74129	22	239			40
Human Bcl-2 protei	AAG64036	22	239	0.	406.5	39
2 prote	AAG64035	22	239	40.3	406.5	38
N	AAE08573	22	239		406.5	37
, _–	AAW87812	20	239	40.3	406.5	36
- 1-2	AAW40217	19	239		406.5	ω U
z ar	AAR71404	16	239		406.5	34
, K	AAR70331	16	239	•	406.5	ω ω
e ge	AAR42312	14	239	•	406.5	32
20	AAP80987	9	239	40.3	406.5	31
•	AAB35130	22	239		408.5	30
bcl-2.	AAB74127	22	239	•	408.5	29
A human BC1-2 prot	AAW87810	20	239	40.5	408.5	28
CL-2.	AAB35131	22	236		409	27
cl-2 pro	AAG64037	22	239	40.9	412.5	26
·	AAB73304	22	233	•	421.5	25
"Deprenyl" (KIM) -1	AAW19396	18	225	41.8	422	24
(3	AAB47515	22	233		424.5	23
Human BCI-xL prote	AAB50538	22	233	42.1	424.5	22
Human Bci-XL prote	AAG64262	22	233	42.1	424.5	21
Human Bci-XL prote	AAY69969	21	233	42.1	424.5	20
Bcl-x polypeptide.	AAY83223	21	233	42.1	424.5	19
	AAW31530	18	233		424.5	18
Bcl-XL protein. H	AAW05821	17	233	•	424.5	17
۲	AAR68887	16	233		٠.	16
e BCL	AAB73303	22	233	42.2	425.5	15
-X1-DTR ap	AAU00219	22	411	•	9	14
oacid	AAW59884	19	365	74.9	756	13
-2.	AAW36048	18	168	7.	7	12

ALIGNMENTS

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AAY05531
                                                                                                                                                RESULT
Mouse Bcl-w protein essential for spermatogenesis.
                                                                        AAY05531;
                                                                                                          AAY05531 standard; Protein; 193 AA.
                                    05-JUL-1999 (first entry)
                                                                                                                                              _
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Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility; animal model

WPI; 1999-243890/20. N-PSDB; AAX25133. 16-SEP-1998; WO9913710-A1 Mus sp. Adams J, Cory S, Gibson L, (HALL-) HALL INST MEDICAL RES WALTER & ELIZA. 16-SEP-1997; 25-MAR-1999. 97AU-0009228. 98WO-AU00764. Koentgen F, Print C;

Claim 2; Page 35; 52pp; English

protein associated with Bcl-w

An animal model exhibiting reduced levels of a Bcl-w protein and/or

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RESULT
AAW61391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
Nucleic acids encoding B-cell lymphoma-y protein - useful for
                               N-PSDB;
                                 WPI; 1998-446079/38.
N-PSDB; V283333.
                                                                                                                              23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                       11-FEB-1997;
                                                                                                                                                                                                  04-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecules and genetic sequences useful for inducting or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
                                                                                                  (COCE-) COCENSYS INC
                                                                                                                                                                                                                             US5789201-A
                                                                                                                                                                                                                                                       Rattus sp
                                                                                                                                                                                                                                                                                  bcl-y; bcl-2;
                                                                                                                                                                                                                                                                                                           Rat bcl-y protein.
                                                                                                                                                                                                                                                                                                                                        02-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                           AAW61391 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                        2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \verb|matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fs \tt dlaaqlhvtpgs aqqrftqvs delfqggpnwgrlvaffvfgaalcaesvnkemeplvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                        ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AA;
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                             cell death pathway; apoptotic; apoptosis; rat.
                                                                                                                             96US-0012201
97US-0798897
                                                                                                                                                                     97US-0798897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.7%;
                                                                                                                                                                                                                                                                                                                                                                                             193
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Pred. No. 5.5e-102;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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В
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                                                                  23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
            Guastella J;
                                                                                                                                                                                                                                                              Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                                                        25-NOV-1997;
                                                                                                                                                                                                            Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW97391;
                                     (COCE-) COCENSYS INC
                                                                                                                                                      16-MAR-1999
                                                                                                                                                                                 US5883229-A.
                                                                                                                                                                                                                                           parasite.
                                                                                                                                                                                                                                                                                                                                                                   The rat bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW97391 standard; Protein; 193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The mammalian bcl-y protein is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activit and the apoptosis blocking activity, bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Alt antisense constructs can be used in disorders where prevention of cell
                                                                                                                                                                                                                                                     Kaposi's sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Fig 3A; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                galvtvgaffask 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALVIVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qvqdwmvtyletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \verb|fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancers
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                               96US-0012201.
97US-0798897.
97US-0978523.
                                                                                                                       97US-0978523
                                                                                                                                                                                                                                                     lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.3%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1002; DB 19;
Pred. No. 1.5e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 193;
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RESULT
AAM97393
ID AAM9
AC AAM9
AC AAM9
AC AAM9
AC AAM9
XX 20-M
XX 20-M
XX Prot
XX Rat
KW Prog
KW head
KW head
KW mult
KW agiin
KW prem
KW prem
KW prem
KW prem
XX Syrum
XX Sy
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                                                                                                                                                                                                                                                                                                                                                                   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y, bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein sequence of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW97393 standard; Protein; 192 AA
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                                                                                                                                               Unidentified
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Pred. No. 1.5e-101;
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RESULT
AAY05530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes rat bol-y protein (Rbbl-y) and human bol-y protein (Hbbl-y). Rbbl-y and Hbbl-y are homologues of the bol-2 protein (C protein (Hbbl-y). Rbbl-y and Hbbl-y are homologues of the bol-2 protein c thought to be involved in programmed cell death (apoptosis and necrosis). Rbbl-y and Hbbl-y proteins may be used to treat conditions associated c with a disruption of the cell death pathway. If they act as cell death c inhibitors, they may be used in therapies to treat subjects suffering c from: strokes, head trauma, Alzheimer's Disease, neural and muscular c degenerative diseases (especially multiple sclerosis), myocardial c degenerative diseases (especially multiple sclerosis), myocardial c degenerative diseases (especially multiple sclerosis) myocardial c dinfarction, vitally induced cell death, aging, spinal cord injuries and c amyotrophic lateral sclerosis conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain c conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune c diseases. They may also be used to cause cell death in, and hence
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X E X D X AC X
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Best Local
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11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel bcl-y homologues of the rat and human bcl-2 protein for modulating programmed cell death % \left( 1\right) =\left\{ 1\right\} =\left\{ 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COCE-) COCENSYS INC.
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                                                                                                                                                                05-JUL-1999
                                               Human Bcl-w protein essential for spermatogenesis.
                                                                                                                                                                                                                                                                                                                                                                                           AAY05530 standard; Protein; 193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 alvtvgaffask 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 vqdwmvtyletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgavalg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 ALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 sdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvgq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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97US-0798897.
97US-0978523.
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Pred. No. 5.3e-101;
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RESULT
AAW61392
                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is human Bcl-w, a pro-survival member of the CC Bcl-2 family which is widely expressed and which is essential for CC spermatogenesis. The invention relates generally to a method of CC molecules and genetic sequences useful for inducing or reducing CC fertility of male animal model for the identification of CC molecules and genetic sequences useful for inducing or reducing CC fertility, or for reducing fertility, by modulating CC spermatogenesis. An animal model carries a mutation is at least CC one allele of the human or murine bol-w gene (see AAX25132-35) or in CC a gene associated with bol-w. Such animals have disorganised CC seminferous tubules and are substantially infertile, but possess no CC other major abnormalities as determined by histological examination. CC They can be used to screen for therapeutic molecules including continuity spermatogenesis in animals, or which can induce
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                   Matches
              02-OCT-1998
                                          AAW61392;
                                                                   AAW61392 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 33; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An animal model exhibiting reduced levels protein associated with \operatorname{Bcl-w}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams
                                                                                                                                       181
                                                                                                                                                                 181 GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatogenesis;
                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                61
                                                                                              6
                                                                                                                                                                                                                                                                                                                  MATPASTPDTRALVADFVGYRLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                       galvtvgaffask 193
                                                                                                                                                                                                      QVQDMMVAXLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                            FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                   matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                         qvqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                  190;
                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cory S,
                                                                                                                                                                                                                                                                                                                                                                                                                                     193
                                                                                                                                                                                                                                                                                                                                                                Conservative
           (first entry)
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                                                                 Protein; 193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gibson L,
                                                                                                                                                                                                                                                                                                                                                                           98.8%;
                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                            Score 997;
Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                             Mismatches
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5.3e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                      Length 193;
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Best Local S
Matches 189
    Rat bcl-y protein;
                             The human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the cell death pathway. The bol-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Als antisense constructs can be used in disorders where prevention of cell
                                                                                        AAW97392;
                                                                                                             AAW97392 standard; Protein;
                                                             20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth {\rm e\cdot g\cdot} cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            death is desired.
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                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                    181 galvtvgaffask 193
                                                                                                                                                                                                                                                    121 QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human bcl-y protein.
                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                             7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammalian bcl-y protein is a member of the bcl-2 family,
                                                                                                                                                                                                                                                                                                                                                                  MATPASTPDTRALVADEVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRT
                                                                                                                                                                                                                 GALVTVGAFFASK 193
                                                                                                                                                                                                                                         qvqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval
                                                                                                                                                                                                                                                                                             FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                     matpasapdtralvedfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1998-446079/38
DB; AAV28334.
                                                                                                                                                                                                                                                                                                                                                                                                                  189;
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                        (first entry)
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97US-0798897.
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     Rbcl-y;
                                                                                                                                                                                                                                                                                                                                                                                                                           98.3%;
97.9%;
human bcl-y protein; Hbcl-y; bcl-2 homologue;
                                                                                                                 193
                                                                                                                                                                                                                                                                                                                                                                                                         Score 992; DB 17,
Pred. No. 1.9e-100;
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Length 193; Indels

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Best Local
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11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis - conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5883229-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents human bcl-y protein (Hbcl-y). The specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Columns 17-18; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-214150/18.
N-PSDB; AAX15946.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COCE-) COCENSYS INC
                                                               181
                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRT 60
                                                                                                                                                                                                                                                                                      FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                \verb|matpasapdtralvedfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt|
GALVTVGAFFASK 193
                                                                                                                     QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                                                                                                                    fs dlaaq 1 hvtp gs aqqrft qvs delf qggpn wgrlvaffvfgaal caes vn kemeplvgalaet ac delfar to the state of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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97US-0798897.
97US-0978523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.3%;
97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 992; DB 20;
Pred. No. 1.9e-100;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                    This sequence represents a novel human protein, bcl-w, encoded by the bcl-2 gene family and extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Upregulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding apoptosis related gene bcl-\mathbf{w} - used or inhibit cell survival, e.g. for treatment of cancer and degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW36047 standard; Protein; 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 48; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1996;
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                           antibody production or screening of potential modulators
 181
                          181
                                                       121
                                                                                   121
                                                                                                               61
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                                                                                                                                                                                              1 MATPASTPDTRALVADEVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
galvtvgaffask 193
                                                                    QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                  \verb|matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1997-489635/45.
             GALVTVGAFFASK 193
                                                       \tt qvqewmvayletrlvdwihssggwaeftalygdgaleearrlregnwasvrtvltgaval
                                                                                                            188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT96577
                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cory S,
                                                                                                                                                                                                                                                                                                  193
                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gibson LM, Holmgreen SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                         98.1%;
97.4%;
                                                                                                                                                                                                                                           Score 990; DB 18;
Pred. No. 3.1e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                       Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to induce
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AAY05532
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Best Local Similarity
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                              The present sequence is described of a derivative of human Bcl-w (see also AAY05530), a pro-survival member of the Bcl-2 family that is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to
                                                                                                                                                                                                                                                                                       screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An animal model exhibiting reduced levels of a Bcl-w protein and/or
 181
                             121
                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HALL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9913710-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Bcl-w protein essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY05532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY05532 standard; Protein; 193 AA.
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                                                                                                                                              1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                          GALVTVGAFFASK 193
                                    QVQDMMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                 \verb|matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt|
                       qvqewmvayletrlvdwihssggwaeftalygdgaleearrlregnwasvrtvltgaval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999-243890/20.
                                                                                                                                                                                                188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HALL INST MEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associated with Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cory S,
                                                                                                                                                                                                                                                                 193 AA;
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97AU-0009228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibson L,
                                                                                                                                                                                                          98.1%;
97.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52pp; English.
                                                                                                                                                                                              Ψ
                                                                                                                                                                                          Score 990; DB 20;
Pred. No. 3.1e-100;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for spermatogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Print C
                                                                                                                                                                                                                     Length 193;
                                                                                                                                                                                           Indels
                                                                                                                                                                                           0;
                                                                                                                                                                                        Gaps
                                                                                                       120
                                                                                                                                    60
                       180
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The present sequence represents a mammalian bcy-l protein.

C The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein (C thought to be involved in programmed cell death (apoptosis and necrosis). C Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death (C inhibitors, they may be used in theraptes to treat subjects suffering C from: strokes, head trauma, Alzheimer's Disease, neural and muscular C degenerative diseases (especially multiple sclerosis), mycoardial confirment, vitally induced cell death, aging, spinal cord injuries and c myotrophic lateral sclerosis- conditions where cells under go premature c lel death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain c viable in culture for an extended period. In contrast, if they act as conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Columns 19-22; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel bcl-y homologues of the rat and for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalian bcl-y protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW97394 standard; Protein; 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 galvtvgaffask 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parasites
192
AA;
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97US-0798897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful
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Query Match
Best Local Similarity
Matches 188; Conserv

Conservative

97.8%; 97.9%;

Score 987; DB 20; Pred. No. 6.6e-100; Mismatches

Length 192; Indels

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Gaps

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                     animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-1999
Sequence
                                                                                                                                                                                                  The present sequence is described of a derivative of mouse Bcl-w (see also AAY05531), a pro-survival member of the Bcl-2 family that is widely expressed and which is essential for spermatogenesis. The derivative lacks the 24 N-terminal amino acids of Bcl-w. The invention relates generally to a method of treatment and to an
                                                                                                                                                                                                                                                                                           Disclosure; Page 39; 52pp; English
                                                                                                                                                                                                                                                                                                                                     An
                                                                                                                                                                                                                                                                                                                                                                                                           Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                       (HALL-) HALL INST MEDICAL RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY05533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY05533 standard; Protein; 192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    animal model exhibiting reduced levels otein associated with Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alvtvgaffask 192
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                                                                                                                                                                                                                                                                                                                                                                              1999-243890/20
                                                                                                                                                                                                                                                                                                                                                                                                          Cory S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-AU00764.
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                                                                                                                                                                                                                                                                                                                                                                                                           Gibson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deritvative
                                                                                                                                                                                                                                                                                                                                                                                                          Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                        WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fertility; infertility;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 186;
                                    This sequence represents a novel protein, bcl-w, encoded by the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or
                                                                                                                                                                                                                 Nucleic acid encoding apoptosis related or inhibit cell survival, e.g. for treat degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW36048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW36048 standard;
                                                                                                                                                                                         Claim 6; Page 50-51; 86pp; English.
                                                                                                                                                                                                                                                                        WPI; 1997-489635/45.
N-PSDB; AAT96578.
                                                                                                                                                                                                                                                                                                                Adams JM,
                                                                                                                                                                                                                                                                                                                                                                   27-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse bcl-w protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1998
Sequence
                            screening
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                                                                                                                                                                                                                                                                                                             Cory S,
                            of potential modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degenerative disease.
  168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                Gibson LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.2%;
                                                                                                                                                                                                                               otosis related gene e.g. for treatment
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                                               Holmgreen
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                                                                                                                                                                                                                                  bcl-w - used to of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT 1
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ADW 9884
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AC AAMS
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KW immu
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XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
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Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergor tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feng
                                                                                                                                                                                                                                                                     used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious age
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-1997;
21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9831800-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AUCK-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW59884 standard;
                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                       1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
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                                                                                                                                                                                                                                                        products can also
                                                                                                                                                                                                                                                                                                                                          is the amino acid sequence of the CDNA clone Bcl-like (HAICH29), in the method of the invention. The products of the clone can be for treating conditions associated with abnormal expression of
1998-414099/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fs dlaaq in \verb|vtpgs| aqqrft qvs delf qggpn wgrlvaffvfgaal caes vn kemeplvg
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                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUCKLAND UNISERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV41925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 97.6
54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gentz RL,
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                            AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0034205.
97US-0034204.
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                                                                                                      74.9%;
97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Krissansen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                     be used for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.6%;
                                                                            Score 756; DB Pred. No. 3.2e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365
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                                                                                                   DB 19;
3.2e-74;
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                                                                                                                          Length 365;
                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergies
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric -
Chimeric -
Chimeric -
                                                                                                           Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, he domains which targets protein to a cell and modifies apoptotic a
                                                                                                                                                                                   Youle
                                                                                                                                                                                                      (USSH)
                                                                                                                                                                                                                                   16-AUG-1999;
                                                                                                                                                                                                                                                     15-AUG-2000;
                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                             diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                                                                                                                                                                                                        22-FEB-2001.
                                                                                                                                                                                                                                                                                            WO200112661-A2.
                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bcl-xl-DTR apoptosis-modifying fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU00219
                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huntington's disease.
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                                                                                                                                                               2001-218343/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVQDWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \verb|matpasapdtralvadfvgyklrgkgyvcgagpgegpaadplhgamraagdefetrfrrt|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bcl-X1-DTR; apoptosis; cancer; spinal muscular atrophy;
                                                                                                                                                       AAS00247
                                                                                                                                                                                                    US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                               HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein;
                                                                                                                                                                                  Liu
                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium diptheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                    2000WO-US22293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                  99US-0149220.
                                                                                                                                                                                                                                                                                                                                                    /note-
254..2
                                                                                                                                                                                                                                                                                                                        260.
                                                                                                                                                                                                                                                                                                                                                                     /note= "10x histidine tag" 21...253
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                  Collier
                                                                                                                                                                                                                                                                                                                                                    . 259
                                                                                                                                                                                                                                                                                                         "DTR, diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                          "Bcl-Xl amino acids 1 to 233"
                                                                                                                                                                                                                                                                                                                                         "Linker amino acids,
                                                                                                                                                                                                                                                                                                                              toxin receptor binding
                                                                                                            cell and modifies apoptotic response
                                                                                                                                                                                                                                                                                                                            linking Bcl-Xl to diphtheria ing domain (DTR)"
                                                                                                                       has two
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The sequence represents the amino acid sequence of Bcl-Xl-DTR apoptosis-modifying fusion protein comprising Bcl-Xl sequence fused via a short linker to diphtheria toxin receptor binding domain (DTR). The functional apoptosis-modifying fusion protein is capable of binding a target cell and integrating into or crossing a cellular membrane of the target cell comprising at least two domains, one of which targets the fusion protein to the target cell and another of which modifies an apoptotic response of

The fusion

protein is

useful

Claim

4;

Page

56-57; 65pp;

English.

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AAB73303
ID AAB
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or enhancing) apoptosis in a target cell, such as neuron, lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or hyper-proliferative cell or an adipocyte. It is also useful for reducing apoptosis in a subject after transient ischaemic neuronal injury, apoptosis in a cord injury. The fusion protein may be used to treat various diseases and injury conditions through inhibition or enhancement of apoptotic cellular response, including neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, spinal muscular atrophy, stroke episodes and unregulated cell growth as in tumours and various cancers. The apoptosis-modifying fusion protein can be delivered effectively throughout the body and targeted to selective tissue and
           Modified cDNA of rat bcl-x gene and encoded protein with membrane permeability to enhance uptake for effective inhibition of cell deat. e.g. apoptosis, useful in remedies for diseases associated with cell death -
                                                                                                                                         Ohta
                                                                                                                                                                                                                                                                                                                                                                                Rat Bcl-xL; apoptosis inhibitor; programmed cell death inhibitor;
wild-type; antiapoptotic; cell death-associated disease;
                                                                                                                                                                       (NISC-) JAPAN SCI & TECHNOLOGY CORP
                                                                                                                                                                                                        17-AUG-1999;
                                                                                                                                                                                                                                     17-AUG-2000; 2000WO-JP05502
                                                                                                                                                                                                                                                                     22-FEB-2001.
                                                                                                                                                                                                                                                                                                     WO200112807-A1
                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                             Rat wild-type Bcl-xL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB73303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB73303 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGALVTVGAFFAS 192
                                                                                          2001-211219/21.
DB; AAF75960.
                                                                                                                                                                                                                                                                                                                                                                 transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                        99JP-0230642
                                                                                                                                                                                                                                                                                                                                                                 preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.6%; Score 429.5; DB 22; 39.5%; Pred. No. 2.1e-38; 39.5%; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22;
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein. The invention also encompasses recombinant vectors and host cells comprising the modified nucleic acid sequence. The mutant BCl x protein is able to permeate the cell membrane, thus enhancing its ability to be taken up into a cell and to act as an inhibitor of apoptosis (programmed cell death). BCl-xFNK and nucleic acids encoding it are useful in remedies for diseases associated with cell death and in additives for maintaining the stability of transplanted cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a mutant rat Bcl-x protein and the cDNA encoding it. The mutant rat Bcl-x protein (Bcl-xFNK) has the substitutions Y22F, Q26N, and R165K relative to the wild-type Bcl-xL substitutions Y22F, Q26N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 45-46; 56pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 organs. The present sequence represents wild-type rat Bcl-xL.
                                      141
                                                                             125
                                                                                                                 81
                                                                                                                                                        66
                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                        11 RALVADFVGYRLRQKGY-----V 28
                                                                                                                                                                                                                                                                                                               Local Similarity
les 92; Conserv
                                                                                                                                                                                                                                   6
                                                                                                                                                                          CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                          SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                         relvvdflsyklsqkgyswsqfsdveenrteapeeteperetpsaingnpswhladspav 65
nggwdtfvdlygnnaaaesrkgqerfnrwfltgmtvagvvllgsl 229
                                                                                                               QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                    nga-tghsssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgtayqsfe 124
                                                                                                                                                                                                                                                                                                                                                                                                              233 AA;
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                   42.2%;
                                                                                                                                                                                                                                                                                                                 23; Mismatches
                                                                                                                                                                                                                                                                                                                                 Score 425.5;
Pred. No. 2.7
                                                                                                                                                                                                                                                                                                               2.7e-38;
ches 57;
                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                               Gaps
```

4

Search completed: June 10, 2002, 10:25:48
Job time: 161 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using sw model

June 10, 2002, 10:26:22; Search time 28.15 Seconds (without alignments) 658.801 Million cell updates/sec

US-09-155-327E-9

Perfect score:

MATPASTPDTRALVADFVGY......LTGAVALGALVTVGAFFASK 193

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq Length: 0

length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_71:* pir1:*
pir2:*

pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	თ	S	4	ω	N	_	NO.	Result
•	147.5	•	154	154	154		169	171	174	179	277.5	342	345.5	353		374.5	375	399	401.5	402	403	408	408.5	411	420.5	421.5	424.5	425.5	score	•
14.6		14.9		15.3	15.3	15.7	6	٠	7.	7	27.5	ω	34.2	35.0	6.	7.	7.	9	39.8	9	9	0	40.5				٠	42.2	Match	
218	179	133	280	261	192	192	211	176	211	170	154	205	199	216	227	214	190	236	233	236	236	236	239	232	233	233	233	233	Length	
2	N	N	2	2	N	2	N	N	2	N	N	-	Н	N	N	N	Ν	ν	ν	1	N	N	_	N	N	2	Ν	2	BG	,
B47538	JC7255	I53295	A53189	н88578	A47538	D47538	S58875	167435	S58873	I49055	158194	TVHUB1	TVMSB1	в37332	JE0203	I49057	A47537	JC7383	167431	TVMSA1	I53744	167432	TVHUA1	S24390	A37332	S51761	B47537	I49056	E	;
0	Bax-delta protein	0	apoptosis suppress	ed-9 [im	bcl-2-associated p	bcl-2-associated p	cdn-2 protein - hu	gene bcl-xshort pr	Bak protein - huma	bcl-x short - mous	_				apoptosis regulato	bcl-x transmembran	apoptosis regulato	B-cell lymphoma 2	BCL-X-Long - rat	transforming prote	gene bcl-2 protein	BCL-2 - rat (fragm			transforming prote		apoptosis regulato	bcl-x long - mouse	Description	1

45	44	43	42	41	40	39	38	37	36	<u>კ</u>	34	33	32	<u>3</u>	30
81.5	82.5	83.5	83.5	83.5	86	86	86.5	86.5	88	105	116	119	138.5	141	144
8.1	8.2	8.3	8.3	8.3	8.5	8.5	8.6	8.6	8.7	10.4	11.5	11.8	13.7	14.0	14.3
886	3430	872	872	358	279	270	3433	301	185	172	350	175	143	255	177
Ν	۲	Ν	N	1	N	N	μ.	N	N	N	Ŋ	N	N	N	2
A32758	GNWVWV	G98026	н95160	AJLCQB	B97381	AI2598	GNWVKV	T36534	B83217	I49449	A47476	I39055	138921	JC7567	S54778
beta-amyloid-like	genome polyprotein	alaninetRNA liga	alanyl-tRNA synthe	glutamateammonia	dihydrodipicolinat	dihydrodipicolinat	genome polyprotein	probable lipase/es	hypothetical prote	hemopoietic-specif	BCL2 homolog MCL1	Bcl-2 related - hu	bcl-2-associated p	Mcl-la protein - z	NR-13 protein - qu

ALIGNMENTS

A;Cross-references: EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g506648 R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M. submitted to the EMBL Data Library, November 1994 A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line th A;Reference number: S52866 A;Accession: S52866 R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.

J. Immunol. 153, 4388-4398, 1994

A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes
A;Reference number: 149055; MUID:95052604

A;Accession: 149056 bcl-x long - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999 C;Accession: 149056; S52866 A; Molecule type: mRNA A; Residues: 1-233 <RES> A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA A; Residues: 1-233 <KAM> A; Cross-references: EMBL: X83574; NID: 965 C; Superfamily: bcl transforming protein A; Status: preliminary EMBL: X83574; NID: g695622; PIDN: CAA58557.1; PID: g695623

Š 밁 οy B Qy Db Qy Query Match Best Local Similarity Matches 185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183 125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184 81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124 29 11 RALVADFVGYRLRQKGY-----6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65 CGAGPGEGPAAD-------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRET 80 92; Conservative 42.2%; Score 425.5; DB 2; 40.9%; Pred. No. 4.3e-32; tive 23; Mismatches 57; ----V 28 Indels Length 233; 53; Gaps 4

RESULT B47537

apoptosis regulator bcl-xL - human N; Alternate names: bcl-2-related protein

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A; Molecule type: DNA
A; Residues: 1-125,189-233 <MI2>
A; Cross-references: EMBL: X82537; NID: g607176;
                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Reference number: S51761 A; Accession: S51761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCL-X protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C;Accession: S51761; S51762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
F;1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Contains: apoptosis regulator bc1-xs
c;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C;Accession: B47537; C47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; 'Cell 74, 597-608, 1993
Cell 74, 597-608, 1993
  A; Introns:
C; Superfam
                                                                                                                                                                                                                                          A; Experimental source: embryonic; brain A; Accession: S51762
                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-233 <MIC>
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                                                                             A; Note: smaller form due to
                                                                                                      A; Experimental source: embryonic; brain
                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g607177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Michaelidis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: BCL2L
A; Cross-references: GDB: 228079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-69,'G',71-125,189-233 <BO2>
A;Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:L20121; NID:g510900; PIDN:CAA80661.1; A;Accession: C47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptoti A; Reference number: A47537; MUID:93364977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown;
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Best Local S
Matches 90
  Superfamily:
                                                       Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 RALVADFVGYRLRQKGY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65
                        125/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-233 <BOI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
bcl transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.1%; Score 424.5; DB 2;
40.2%; Pred. No. 5.3e-32;
tive 24; Mismatches 59;
                                                                                splicing
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                         November 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translated from GB/EMBL/DDBJ
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                                                                                                                                    PIDN:CAA57887.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VCGAGP----GEGPAA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229
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                                                                                                                                 PID:g607178
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A;Introns: 189/3
C;Superfamily: bcl transforming protein
C;Keywords: mitochondrion; transforming protein; transmembrane protein
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(;Speciles: Gallus gallus (chicken)

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997

C;Accession: A37332; S35453

C;Accession: A37332; S35453

R;Eguchi, Y; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A;Title: Isolation and characterization of the chicken bcl-2 gene: expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
A37332
S24390
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C; Genetics:
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A; Residues: 1-233 <EGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A37332; MUID:92375724 A; Accession: A37332
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                                                                                                                145
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                                                                            190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                      42
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                                                                                                                                                                                                                                70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
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                                                                                                                                                                                                                                                                                                                                                9 DTRALVADFVGYRLRQKGYVCGAG-----PGEGPAADP------
                                                                                              AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                              ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWWVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQENG
                                                                                                                                                      ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW
                                                                                                                                                                                                                                                                                                          DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGPGEGPAAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAVNG
                                                                                                                                                                                                                                                                    ------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
                                                                                                                                                                                                                                                                                                                                                                                                    h 41.7%;
Similarity 37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: D11381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                    33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Score 420.5; DB 2
Pred. No. 1.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 421.5; DB Pred. No. 1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bcl-2 gene: expression
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                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                        189
                                                                                                                                                                                                                                129
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transforming protein (Bcl-2) homolog - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999

C;Accession: S24390 R;Cazals-Hatem, D.L.;

Biophys.

Acta

; Louie, ta 1132,

D.C.; Tanaka, 109-113, 1992

s.;

Reed, J.C

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R:Tsujinoto, Y: Croce, C.M.

R:Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

R:Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, and protein products of bcl

R:Ritle: Analysis of the structure, transcripts, and protein products of bcl

R:Reference number: A29409; MUID:86259760

R:Rolecule type: mRNA

A:Residues: 1-95, 'A', 97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

A:Residues: 1-95, 'A',97-109, 'G',111-236, 'S',238-239 <TSU>
A:Rolecule type: mRNA

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A;Accession: S24390
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-232 <CAZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 15-Oct-1999
C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
R;Eguchi, Y:; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression; R;Reference number: A37332; MUID:92375724
A;Accession: C37332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-239 <EGU>
A; Note: this report is a correction
R; Tsujimoto, Y.; Croce, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVHUA1
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A; MoLecule type: mRNA
A; Residues: 1-58,'T',60-116,'R',118-239 <CLE>
A; Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
R; Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J
Oncogene Res. 2, 263-275, 1988
                                                                                                                                                                                                     R:Cleary, M.L.; Smith, S.D.; Sklar, J.
Cell 47, 19-28, 1986
A;Title: Cloning and structural analysis of cDNAs
A;Reference number: A24428; MUID:87002488
A;Accession: A24428
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                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-239 <SET>
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Best Local S
Matches 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFRDGVNWVRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPSPPARL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTRALVADFVGYRLRQKGYVCGAG-----PGEGPAADP------
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                                                                                                                                                                                                                                                                                                   for
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                                                                                                                                                                                                                                                                                               bc1-2
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                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          products of bcl-2,
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                                                                                                                                                                                                                                                                                                   a hybrid bcl-2/immunog
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                                               J.J.; Bakhshi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P.; Korsmey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
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VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS

-----VCGAGPGEGPAADPLHOAMRAAGDEFETRERRTESDLAAOLHUTPGSAQQRETQ 81

DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRRAPTPGIFSFQPESNRTPAVHRDTAART

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A;Description: blocks apoptosis in hematopoietic cells C;Superfamily: bcl transforming protein C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma;
                                                                                                                                                                                                                                                                                           R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology 136, 232-241, 1995
A;Tille: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: I53295; MUID:95129487
                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26
C:Accession: I67432
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A;MoLecule type: DNA
A;Residues: 1-6, 'Z', 8-58, 'T', 60-128, 'C', 130-239 <HUA2>
A;Residues: 1-6, 'Z', 8-58, 'T', 60-128, 'C', 130-239 <HUA2>
A;Note: the sequence was determined from the germline gene
C;Comment: Constitutive expression of BCL2 following t(14:18) chromosomal translocati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphom A;Reference number: A27622; MUID:88217344
A;Accession: A27622
Qy
                                                                                                                                                          A;Cross-references: EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; PID:g1004379 C;Superfamily: bol transforming protein
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A; Map position: 18q21.3-18q21.3
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A; Residues: 1-58, 'T', 60-239 < HUA>
                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-236 < RES>
                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity

    rat (fragment)

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Pred. No. 1.8e-30
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                                                    Mismatches
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A; Residu
C; Geneti
A; Gene:
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                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
C;Accession: A25960; E37332
R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
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                                                 A; Molecule type: DNA
A; Residues: 1-33, 'E'
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A; Residues: 1-236 <NEG>
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A; Residues: 1-236 <RES>
A; Cross-references: GB:L14680;
                                                                                         A;Status: preliminary; nucleic acid sequence not
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                                                                                                                                                                                                                                                                                                                                    A; Reference number: A90893;
                                                                                                                                                                                                                                                                                                                                                             A; Title: Molecular analysis
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29-May-1998 #sequence_revision 29-May-1998
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291-292, 1994
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35.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-233 < RES>
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85; Conser
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B-cell lymphoma 2 protein - Chinese hamster C;Species: Cricetulus griseus (Chinese hamst C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #sequence_revision 17-Nov-2000;Accession: JC7383 R;Tomicic, M.T.; Christmann, M.; Kaina, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: I53295; MUID:95129487
A;Accession: I67431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCL-X-Long - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
C;Accession: 167431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 192/3
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; mitochondrion; transforming protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: bcl transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
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                                                                                                                                                                                                                                                                                                                                                                                QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                                   QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                    NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE 124
                                                                                                                                                                                                                                  NGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLS-LPWVGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 401.5; DB 2;
Pred. No. 7.3e-30;
""matches 61;
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Pred. No. 6.7e-
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17-Nov-2000
                                                    #text_change
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Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A;Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A;Reference number: JC7383
A;Contents: Ovary
A;Accession: JC7383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: bcl transforming protein
C;Keywords: B-cell lymphoma; ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Comment: \ This \ protein \ has \ anti-apoptotic function, and supports cell survival <math display="inline">C; Genetics:
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A; Residues: 1-236 <TOM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: A47537
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; T
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A;Residues: 1-190 <BOI>
A;Cross-references: GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1; PID:g510899
C;Superfamily: bcl transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A47537; MUID:93364977
A; Accession: A47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART 69
                                                                            126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSOLHLTPFTARGREAT 129
186 R-TAL: 189
                                         146 EFTAL 150
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                                                                                                                                                                                                                                                                                   86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                           66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125
                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L.H.; Gonzare
597-608, 1993
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                                                                                                                                                                                                    -----AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                                                                                                                                                                                                                                           RELVIDEVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65
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                                                                                                                                                                                                                                                                                                                              80; Conservative
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                                                                                                                                                                                                                                                                                                                                                  37.2%; Score 375; DB 2; Length 190; 43.2%; Pred. No. 1.7e-27;
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R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.

J. Immunol. 153, 4388-4398, 1994

A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes

A;Reference number: 149055; MUID:95052604

A;Accession: 149057

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I49057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bcl-x transmembrane deleted - mouse
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A; Residues: 1-214 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U10102; NID:g506649; PIDN:AAA82174.1; PID:g506650
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C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999
C;Accession: JE0203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis regulator bcl-x isoform - human N;Alternate names: h-bcl-xbeta
                                                                                                                                                                                                                                                                                                                                                                                                                 R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E. Biochem. Biophys. Res. Commun. 248, 147-152, 1998
A;Title: Identification of a human cDNA encoding a novel bcl-x isoform. A;Reference number: JE0203; MUID:98340865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JE0203
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                                                                                     QΥ
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C; Superfamily: b
                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:U72398; NID:g1622940; PIDN:AAB17354.1; PID:g1622941
                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-227 <BAN>
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                                                                                       11 RALVADFVGYRLRQKGY------
                                                                                                                                                         Local
29 CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                            6 RELYVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65
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bcl transforming protein
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                                                                                                                                                         36.8%; Score 371.5; DB 40.3%; Pred. No. 4.3e-27
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Search completed: June 10, 2002, 10:26:22 Job time: 170 sec
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C;Species: Gallus gallus (chicken)
C;Decies: O3-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Apr-1998
C;Accession: B37332; S35452
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie A;Reference number: A37332; MUID:92375724
A;Reference number: A37332; MUID:92375724
A;Accession: B3733
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-216 <EGU>
A;Cross-references: EMBL:D11381; EMBL:D11382
C;Superfamily: bcl transforming protein
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Best Local s
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                                                                                                                                                                                                                                                                                                                                                                                                                    / Match
Local Similarity 37.8%; Score 353; DB 2; Length 216;
Local Similarity 37.8%; Pred. No. 2.1e-25;
Nes 70; Conservative 22; Mismatches 49; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                            9 DTRALVADFVGYRLRQKGYVCGAG------PGEGPAADP---------41
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66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Database :
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SwissProt_40:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

33 33 33	16 17 19 20 21 22 23 24 25 26	113 113 114 115	Result
116 105 99.5 98.5 98.5	175.5 174 156.5 155.5 155.5 154 154 147.5 140.5 138.5 116	1006 997 647 429.5 428.5 425.5 425.5 426.5 420.5 410.5 410.6	Score
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yright. It is produced of Bloinformatics and Institute. There are notions as long as its capreement (See http://wisb-sib.ch).	PRT; 193 AA. d) sequence update) annotation update) annotation update) annotation update; i; Craniata; Vertebrata; i; Sciurognathi; Muridae; bil287; auang D.C., Bernard O., Calling D.C., Calling D.C., Bernard O., Calling D.C.	ALIGNMENTS	SQHC_BRAJA POLIG_KUNJM GLNA_LACSA POLIG_WNV AA_DROME PORA_PYRFU YJ94_ARCFU YJ94_ARCFU YJ45_MYCTU FOLIG_JAEYJ PHCA_SYNP6
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Q92843;
Q1-NOV-1997
                                                                           MEDLINE-97191544; PubMed-9039502;
Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,
Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
"Prediction of the coding sequences of unidentified human genes.
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced analysis of cDNA clones from cell line KG-1 and brain.";
DNA Res. 3:321-329(1996).
                                                                                                                                                                                     Oncogene
                                                                    - i -
                                                                                                                                                                                            Gibson L., Holmgreen S.P., Huang D.C., Bernard O., C. Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., "bcl-w, a novel member of the bcl-2 family, promotes Oncogene 13:665-675(1996).
                                                                                                                                                                                                                                                                                                              Apoptosis regulator Bcl-W. BCL212 OR BCLW OR KIAA0271.
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SEQUENCE
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01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                               FUNCTION: PROMOTES CELL SURVIVAL.
SUBCELLULAR LOCATION: CYCOPLASMIC.
TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES
IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON
           AND SALIVARY GLAND
DOMAIN: BH4 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192;
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85
136
193 AA;
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                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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104 E
151 E
20790 MW;
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99.5%;
                                                                                                                                                                                                                                                                                                                                                                    Created)
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           SEEMS TO
                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1006;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH4.
BH1.
BH2.
; 36CA185F5945DFB4 CRC64;
                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
           ΒE
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           INVOLVED
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                                                                                                                                                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                                                                           update)
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.8e-82;
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           THE
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                                                                                                                                                                                                        Copeland N.G., i., Cory S.; es cell survival.";
           ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT 3
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                Matches 190;
                                                                                                                                AR1_XENLA
Q91827;
                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence updated)
01-NOV-1997 (Rel. 35, Last annotation upo
Apoptosis regulator R1 (XR1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license are not removed.
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
TISSUE-Head;
         SEQUENCE FROM
                              Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00337; BCL;
SMART; SM00265; BH4;
PROSITE; PS50062; BCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00452; Bc1-2; Pfam; PF02180; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002475; BCL2_f
InterPro; IPR003093; BH4.
InterPro; IPR000712; BC1_2.
                                                                         kenopus laevis (African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                                                          <del>--</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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                                                                                                                                                                                                    GALVTVGAFFASK 193
                                                                                                                                                                                                              GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                   FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601931;
                                                                                                                                                                                                                                                                                          FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                     MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q07817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D87461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS01080;
PS01258;
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85
136
193 AA;
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                                         Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1MAZ
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BAA19666.1;
                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; BH4_1;
; BH4_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         вн1;
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104 B
151 B
20774 MW;
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                                                                                                                                                                                                                                                                                                                                                                                         98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                             Score 997; DB 1;
Pred. No. 1.1e-81;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                           BH2.
; 3792243A50281761 CRC64;
                                                                            frog)
                                                                                                                                             228
                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                  Length 193;
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(BH2).
(BH4).
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Gene 158:171-179(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - SUBCELLULAR LOCATION: Membrane-bound (potential).
- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE BRAIN OF MID-METAMOREPHOSIC TO POST-METAMORPHOSIC TADPOLES AND ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95331613; PubMed=7607538; Cruz-Reyes J., Tata J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                   BCLX_CHICK STANDARD; PRT; 229 AA. 007816; Q98908; 01-FEB-1995 (Rel. 31, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                CHICK
                                  Apoptosis regulator Bcl-X.
BCL2L1 OR BCLX OR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 TRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69
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FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.

CUBCELLILLAR LOCATION: Membrane-bound (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRALVEDLVRYKLCQRSLV---PEPSGAASCALHSAMRAAGDEFEERFRQAFSEISTQIH 104
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Pr00452; Bcl-2; 1.
Pr02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q07817; 1MAZ
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SM00265; BH4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207
        (Chicken)
                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139
186
227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.2%;
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Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                  229
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                                                                                                                                                                                                                                                                                                  ΑA
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5.
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SOCCED STREET ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of apoptotic cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (SHORT FORM).
MEDLINE=93364977; PubMed=8358789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spermatogenesis.";
Mol. Reprod. Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vilagrasa X., Mezquita C., Mezquita J.; "Differential expression of bcl-2 and bcl-x during chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=HUBBARD WHITE MOUNTAIN; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97264485; PubMed=9110311
                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 223110; CAA80657.1;
EMBL; U26645; AAB07677.1;
PIR; A47537; A47537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified
                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P53563; 1AF3
                                                                                                                                                                                                                                        PROSITE;
  SEQUENCE
                                                      VARSPLIC
                                                                                   TRANSMEM
                                                                                                             DOMAIN
                                                                                                                                      DOMAIN
                                                                                                                                                          DOMAIN
                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR003093; BH4.
Interpro; IPR000712; Bcl_2.
                                                                                                                                                                                                                    Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR002475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION. INTACT BHI AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
APOPTOTIC ACTIVITY (BY SIMILARITY).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reprod. Dev. 47:26-29(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and this statement is not removed.
                                                                                                                                                                                                                                                                        PS01259;
PS01260;
                                                                                                                                                                                                                                                                                                                           PS01080;
PS01258;
                                                                                                                                                                                                                                                 PS50063;
                                                                                                                                                                                                                                                                                                                                                                               PS50062;
                                                                                                                                                                                                                       Transmembrane;
     229 AA;
                                                                                                                                                                                                                                                 BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                               BCL2_FAMILY;
                                                                                                                                                                                                                                                                                                          BH3;
                                                               144
191
223
229
        25733 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۲.
                                                                                                                                                                                                                             Alternative
     LSRK -> VRTALP (IN SHORT ISOFORM).
A97D3A4D04C0E9DA CRC64;
                                                         ERFYDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLLGSL
                                                                                                                  BH2
                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
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RESULT
BCLX_PIG
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                                                                                                                                                                                       -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis (By similarity). The cleaved protein, lacking the BH4 domain, has propoptotic activity (By similarity).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
EMBL; AJ001203; CAA04597.1; -. HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myocardium of pig.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Expression of apoptosis-associated genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bartling B., Hoffmann J., Holtz J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis regulator Bcl-x.
BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCLX_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 RFVDLYGNNA----AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWE 185
                                                                                                                                                                                                                                                                                                                                                                                                  caspasss (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR DOMAIN: The RHA Arms: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 -----AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 RALVADFVGYRLRQKGY------ 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.6%; Score 429.5; DB 1
41.2%; Pred. No. 3.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schulz R., Heusch G., Dangenes in hibernating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Darmer D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stunned
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BCLX_MOUSE STANDARD;

ID BCLX_MOUSE STANDARD;

AC Q64373; Q60657; Q60658; Q61338;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
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TISSUE=Pre-B cell;
         SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TM))
                                                                      Thompson C.B., Nunez G., "Control of the major bcl-x mRNA form expressed during development and its product localizes to mitochondria. Development 120:3033-3042(1994).
                                                                                                                                                                                 Gonzalez-Garcia M., Perez-Ballestero R., Ding L., Duan L., Boise L.H.,
                                                                                                                                                                                                                            STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=95331139; PubMed=7607090;
                                                                                                                                                                                                                                                                                                                                   Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=2A4B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis regulator Bcl-x.
BCL2L1 OR BCL2L OR BCLX.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA))
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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DOMAIN
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PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
InterPro; IPR000712; BC1_2.
Pfam; PF00452; BC1_2; 1.
Pfam; PF02180; BH4; 1.
CMARK CONTROL OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00337; BCL; 1
SMART; SM00265; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 QVLNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 RALVADFVGYRLRQKGY-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS01080;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26061 MW; 18BF6FA0441912B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 428.5; DB 1; Length 233; Pred. No. 4.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH2.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L.,
Ohta S., Seldin M.F., Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt "A} novel Bcl-x isoform connected to the T cell receptor regulates apoptosis in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM X (BETA)).
STRAIN-C57BL/6 X CBA; TISSUE-Thymus;
MEDLINE-98051053; PubMed-9390687;
Yang X.-F., Weber G.F., Cantor H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95052604; PubMed=7963517; Fang W., Rivard J.J., Mueller D.L., Behrens T.W.; "Cloning and molecular characterization of mouse bcl-x in
                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=97289584; PubMed=9144489;
                  EMBL;
EMBL;
EMBL;
HSSP;
                                                                                  EMBL;
                                                                                                                     EMBL;
                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunity 7:629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lymphocytes."
                                                                                                                                                                          EMBL;
                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic organization, promoter region analysis, localization of the mouse bcl-x gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunol. 153:4388-4398(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPLICING.
TISSUE SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoform promotes apoptosis.

SUBUNIT: BCL-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By SIBUNIT: BCL-x(L) forms heterodimers with BAX does not seem to be similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity).

SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).

ALTERNATIVE PRODUCTS: 4 ISOFORMS; BCX-X(L) (SHOWN HERE), BCL-X(S), BCL-X(BTA) AND BCL-X(DELTA-TM); ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                               with other Bcl2 family members and for repression of cell pTM: Proteolytically cleaved by caspases during apoptosis similarity). The cleaved protein, lacking the BH4 domain, apoptotic activity (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: The BH4 domain is required to
The BH1 and BH2 domains are required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: BCL-X(BETA)IS EXPRESSED IN BOTH EMBRY(POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND POSTNATAL TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to it and preventing the release of the caspase cytochrome c, from the mitochondrial membrane. T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channnel (VDAC) by binding
                           X83574; CAA58557.1;

L35049; AAA51039.1;

L35048; AAA51040.1;

L15048; AAA5174.1;

U10102; AAA82174.1;

U10101; AAA82173.1;

U10100; AAA82173.1;

U10100; AAA82172.1;

U10100; AAA860.1;

U78031; AAB96881.1;

U78031; AAB96881.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Potent inhibitor of cell death.
                                                                                                                                                                                                                                                                                               SWISS\text{-PROT} entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
MGI:88139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE IN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) AND BCL-X(DELTA EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES THAT HAVE BEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158:4750-4757(1997).
 Bc121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain is required for anti-apoptotic activity
                                                       . . . . . . . . . . . . .
                                    JOINED.
                                                                                                                                                                                                                          moved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                             There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for both heterodimerization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhibits
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Bcl-x(S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND BCL-X(DELTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome
                                                                                                                                                                                                                                                                                 restrictions
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 Query Match
Best Local S
Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM PROSITE;
                                                                                                                                                                                  P53563; Q62678; P70614; P70613; Q62836; Q64087; 
01-QCT-1996 (Rel. 34, Created) 
01-NQV-1997 (Rel. 35, Last seguence update) 
16-QCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00452; Bc1-2;
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1
SMART; SM00265; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptosis; Mitochondrion; DOMAIN 4 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003093; InterPro; IPR000712;
                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                             Apoptosis regulator Bcl-x. BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
 Submitted
                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                BCLX_RAT
          Wesselingh S.L.,
                     TISSUE=Brain;
                                  SEQUENCE FROM N.A.
                                                        Submitted
                                                                   Michaelidis
                                                                                TISSUE=Brain;
                                                                                          SEQUENCE FROM N.A.
                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                          185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 RALVADFVGYRLRQKGY-----V 28
                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                     SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                         NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                   NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                                                                                                                         CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                      QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 40.9
92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50062; BCL2
PS01080; BH1;
PS01258; BH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS01260; BH4_1; 1. PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS01259;
h S.L., David G.L., Choi S., Veliuona
(JUN-1995) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002475; BCL2_family.
                                                        is T.M.;
(DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
129
180
180
210
126
189
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                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCL2_FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24
100
148
195
226
188
233
                                                                                           (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26132
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                                                         6
                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 425.5; DB 1
Pred. No. 7.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
MISSING (IN ISOFORM BCL-X(5)).
DTFVDLYGNNAAAESRKGQERFWRWFLTGMTVAGVVLLGSL
FSRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X(DELTA-TM)).
24D2AC79887E072E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK -> GHDCGWCGSAGLTLQSEVTRH (IN ISOFORM BCL-
                                                                                           X(L) AND X(S)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL-X(BETA))
                                                                                                                                                                                                                                  PRT;
                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                  233 AA
             Veliuona M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splicing; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                          databases
 databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
             Hardwick J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                              Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   65
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-I- ALTERNATIVE PODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S)
AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
-ITISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
OWARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
DETECTABLE LEVEL OF BCL-X(S).

-I- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
The BH1 and BH2 domains are required for both heterodimerization
with other Bcl2 family members and for repression of cell death.
-I- PTM: Proteolytically cleaved by caspases during apoptosis. The
cleaved protein, lacking the BH4 domain, has pro-apoptotic
activity (By similarity).
-I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                            EMBL;
EMBL;
                                                                                                                                                                                                          the buropease agreement is not removed. Usage by and this statement is not removed. Usage by and the statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the modified and this statement is not removed. Usage by and the first provided the modified and this statement is not removed.
                                                                                    EMBL;
                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ol "An additional form of rat Bcl-x, Bcl-xbeta, generated by an unspliced RNA, promotes apoptosis in promyeloid cells."; J. Biol. Chem. 271:13258-13265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.; "Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulos cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [3] SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Crystal structure of rat Bcl-xL. Implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aritomi M., Kunishima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS). MEDLINE=98010630; PubMed=9346936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95129487; PubMed=7828536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96278736; PubMed=8662675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol.
                                   L; X82537; CAA57886.1; -.
L; X82537; CAA57887.1; -.
L; U10579; AAA19257.1; -.
L; U72350; AAB17353.1; -.
L; U72349; AAB17352.1; -.
L; U34963; AAA77686.1; -.
L; U34963; AAA77687.1; -.
L; S76513; AAC60701.1; ALT_INIT.
L; S78284; AAC60702.1; -.
                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the E European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-x(S) and Bcl-x(beta) isoforms promote apoptosis.

SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 sthmilarity). Heterodimerization with BAX deem to be required for anti-apoptotic activity (By similarity).

SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bc1-2 protein family.";
Biol. Chem. 272:27886-27892(1997).
FUNCTION: Potent inhibitor of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Potent inhibitor of cell death. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channel (VDAC) by binding the transfer the colors of the content of the colors of the colors.
                      1AF3;
IPR002475;
                      07-JUL-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISOFORMS X(L) AND X(S)).
BCL2_family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inohara N., Ishibashi Y., Ohta
                                                                                                                                                                                                                                                                                                                                                           through
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                                                                                                                                                                                                                                                                                                                                         EMBL
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                                                                                                                                                                                                                                                                                                                                                             a collaboration
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Best Local
                                                                                                            Q07817; Q92976;
01-FEB-1995 (Rel. 31, C
01-FEB-1995 (Rel. 31, L
01-MAR-2002 (Rel. 41, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PROSITE; PS50062; BCL2_PAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4—1; 1.
PROSITE; PS01260; BH4—2; 1.
                                                                                    Apoptosis regulator Bcl-x.
BCL2L1 OR BCL2L OR BCLX.
Homo sanian. ("..."
                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
CONFLICT
SEQUENCE
 SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
MEDLINE=93364977; PubMed=8358789;
Boise L.H., Gonzalez-Garcia M., Postema C.E.
Turka L.A., Mao X., Nunez G., Thompson C.B.;
                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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                                                  NCBI_TaxID=9606;
                                                                                                                                                       BCLX_HUMAN
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                                                                                                                                                                                                        NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                           SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                              QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWWVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                     NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                          CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                             RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
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                                                                                                                                                                                                                                                                                                                                                                                Similarity
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233 AA;
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Gonzalez-Garcia M., Postema Mao X., Nunez G., Thompson
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64
81
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143
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BH4; 1.
                                                                                                                                                       STANDARD;
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Bcl_2.
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                                                                                                                      Last sequence update)
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FSRK -> VRTTPLVCPPLVCLSSVEIPNCPFWSPGMVVED
IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
R -> Q (IN REF. 1).
F -> S (IN REF. 2).
A -> E (IN REF. 2).
A -> U (IN REF. 4).
FF -> SS (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                      23; Mismatches
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BH2.
POTENTIAL.
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Pred. No. 7.
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-> P (IN REF. 4).
2B62B6C63864BC8F CRC64;
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          L., Lindsten
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Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J., Thompson C.B., Fesik S.W.; "Structure of Bcl-xL-Bak peptide complex: recognition between regulators of apoptosis."; Science 275:983-986(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clem R.J., Cheng E.H. Y., Karp C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLEAVAGE BY CASPASES, AND MUTAGENESIS OF MEDLINE=98118550; PubMed=9435230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        x-ray crystallography (2.2 angstroms), and structure medline=96256675; pubMed=8692274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J. Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "bcl-x, a bcl-2-related of apoptotic cell death. Cell 74:597-608(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Modulation of cell death bx Bcl-xL through caspase interaction."; Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).
-:- FUNCTION: Potent inhibitor of cell death. Inhibits activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi A., Kastan M.B., Griffin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muchmore S.W., Sattler M., Liang H., Meadows R.P., Ha Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 381:335-341(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Korsmeyer S.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Multiple Bc1-2 family members demonstrate selective dimerizations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.L.,
                                                                                                                                                       apoptotic activity.

apoptotic activity.

SUBCELLULAR LOCATION. MITOCHONDRIAL MEMBRANES AND PERINUCLEAR SUBCELLULAR LOCATION. MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S) AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADDUT BRAIN.

LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADDUT BRAIN.

LONG-LIVED POSTMITOTIC CELLS, SUCH AS DOUT BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Potent inhibitor of cell death. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channnel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-x(S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoform promotes apoptosis.
SUBUNIT: Bcl-x(L) forms het
SIMILARITY:
SIMILARITY:
                                                                                                          The BH1 and BH2 domains are required for both heterodimerization with other Bc12 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heterodimerization with BAX does
                                                      activity
                                                                             cleaved protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E.H.-Y., Levine
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CONTAINS
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                                                                                lacking the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         в.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heterodimers with BAX does not seem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human Bcl-xL, an inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L.H.,
                                                                          by caspases duri
BH4 domain, has
  HOMOLOGY DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sch D.G., Ueno K.,
Earnshaw W.C., Veliuona M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASP-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAX, B
  1 (BH1).
1 2 (BH2).
                                                                                pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAK and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harlan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harlan J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAK and Bcl-2 required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wong
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CONFLICT
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                    MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                 SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50062; BCL2_FAMILY; PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                          SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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- SIMILARITY:
- SIMILARITY:
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; 1LXL; 21-APR-97.
; 1MAZ; 21-APR-97.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z23116; CAA80662.1;
Z23115; CAA80661.1;
U72398; AAB17354.1;
                                                                RALVADFVGYRLRQKGY - - -
NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                       CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                          RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00337; BCL; 1.
SM00265; BH4; 1.
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS01260; BH4_1; 1. PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS01259; BH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003093;
IPR000712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002475;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion;
                                                                                                                                          233 AA;
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86
129
180
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126
189
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                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                      189
70
                                                                                                                                                                                     138
148
156
176
189
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137
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226
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188
233
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                                                                                                 42.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Alternative splicing; Transmembrane;
                                                                                                                                           WW;
                                                                                      23;
                                                                                    Score 424.5; DB
Pred. No. 9.2e-31
3; Mismatches 5
                                                                                                                                              BY ABOUT HALF.
D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
G -> A (IN REF. 1; CAA80661).
                                                                                                                                                                                             ACTIVITY.

G->A: NO HETERODIMERIZATION WITH BAX.
G->E: NO HETERODIMERIZATION WITH BAX.
D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
                                                                                                                                                                                                                                                                VNW->AIL:
                                                                                                                                                                                                                                                                                                                                                      CLEAVAGE BY CASPASE-1.
MISSING (IN ISOFORM BCL-X(S))
                                                                                                                                                                                      WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
                                                                                                                                                                                                                                                      GRI->ELN: LOSS OF ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                     FRD->VRA:
                                                                                                                                                                                                                                                                                                  CASPASE-3
                                                                                                                                                                                                                                                                                                                     VGDVDS (IN ISOFORM BCL-X(BETA))
                                                                                                                                                                                                                                                                                                                                DTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
FSRK -> VRTKPLVCPFSLASGQRSPTALLLYLFLLCWVI
                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                           E09D3CDD851AE9BE CRC64;
                                                                                                                                                                                                                                                                                                            NO CLEAVAGE
                                                                                                                                                                                                                                                                           NO HETERODIMERIZATION WITH LOSS OF ANTI-APOPTOTIC
                                                                                                  DB 1;
e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage by
                                                                                                                                                                                                                                                                                                            BY CASPASE-1 NOR BY
                                                                                                          Length
                                                                                      Indels
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Q00709;
01-APR-1993 (Rel. 25, 01-APR-1993 (Rel. 25, 16-CT-2001 (Rel. 40, 
                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eguchi Y., Ewert D.L., Tsujimoto Y.;

"Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=B-cell lymphoma;
MEDLINE=92379084; PubMed=1511008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cazals-Hatem D.L., Louie D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=92375724; PubMed=1508712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptosis regulator Bcl-2.
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adult and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125
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                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exeuropean Bioinformatics Institute. There are no restricted to the control of 
                                                                                                                                                                                                                                                                                                                                 DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RaF-1 (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kidney,
thymus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bcl-x(L). Heterodimerization with BAX requires intact BHI and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity) SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen. Kidney, heart, ovary and brain, with the highest levels in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thymus. In the embryo, highly levels expressed in all tissues high levels in the bursa of Fabricius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
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Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last
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on update)
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                                                                      (See http://www.isb-sib.ch/announce/
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                                                                                                                                                as its content
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                                                                                                             Usage
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                                                                                                             by and for
                                                                                                                                                                                    restrictions
                                                                                                                                                                                                                   EMBL outstation
                                                                                                                                         st
                                                                                                                                                                                                                                                          a collaboration
                                                                                                                                                in
                                                                                                             commercia.
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RESULT 10
BCL2_BOVIN
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D11382; BAA01978.1; -
EMBL; D11381; BAA01978.1; J
EMBL; Z11961; CAA78018.1; -
PIR; A37332; A37332,
PIR; S24390; S24390.
HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
SEQUENCE
Reyes R.A., Cock
"Bovine leukemia
                   STRAIN=HOLSTEIN; TISSUE=Thymus;
                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seg
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                     BCL2_BOVIN
002718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis;
DOMAIN
                              SEQUENCE FROM N.A.
                                                            Bovidae;
                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                        Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                NCBI_TaxID=9913;
                                                                                                              Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00337; BCL; SMART; SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                     145
                                                                                                                                                                                                                                                        130
                                                                                                                                                                                                                 190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                                           85
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                                                                                                                                                                                                                                   AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                         ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                     DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAAAAAAAAAASASSHHRPEPPGSA 69
                                                                                                                                                                                                                                                      ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW
                                                                                                                                                                                                                                                                                              AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50062;
PS01080;
PS01258;
                                                            Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS01259;
PS01260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50063;
                                                                                                             regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002475; BCL:
IPR003093; BH4
                                                                                                                                                                                                                                                                                                                                                                                                                           121
139
233 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Mitochondrion
          Cockerell G.L.
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                               STANDARD;
virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H4; 1.
BCL2_FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                             121
139
25687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
149
196
228
64
82
                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                               Bc1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCL2_family
                                                                                                                       Last annotation
                                                                                                                                 Last sequence update)
associated-leukemogenesis is correlated
                                                                                                                                                                                                                                                                                                                                                                                      .68
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Pred. No. 2.1
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G -> V (IN REF. 2).
; 5252555ACB6E4C3D
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E -> S (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSAAASEVPPAEGLRP
                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                233;
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
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use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Bcl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with suppression of programmed cell death and increased expression of nal-2 ".
                                                                                                                                                                                                                                                                                                                    SMART; SM00337; BCL; SMART; SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U92434; AAB53319.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---
SEQUENCE
                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                           PROSITE;
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                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                   MOD_RES
                                                        TRANSMEM
                                                                          DOMAIN
                                                                                              DOMAIN
                                                                                                               DOMAIN
                                                                                                                                 DOMAIN
                                                                                                                                                                    DOMAIN
                                                                                                                                                                                    Apoptosis;
                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).

PTM: Profeolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).

FM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle(By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity). SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and BCl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity). SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Regulates cell death by controlling the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                     PF00452; Bc1-2; 1. PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q07817;
                                                                                                                                                                                                          PS50063;
                                                                                                          ; Transmembrane; N
10 30
64 68
69 72
83 97
                                                                                                                                                                                                                                                                                                                                                                                        IPR002475; BCL2_family.
IPR003093; BH4.
IPR000712; Bc1_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1MAZ
                                                                                                                                                                                                        BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                                                               вн2;
                                                                                                                                                                                                                                             BH3;
                                                                                                                                                                                                                                                                                  BH1;
                                                                                                                                                                                                                                                                                                BCL2_FAMILY;
                                                      145
192
223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rmatics Institute. There are no restrictions on institutions as long as its content is in no
 25099
                                                                                                                                                                                    Mitochondrion; Phosphorylation
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                                                                                                          POLY-PRO.
POLY-ALA.
BH3.
BH1.
BH2.
CLENTIAL.
CLEAVAGE (BY CASPASES) (BY SIMILARITY).
PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
ADIDDOAF98FFF11D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
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20
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P49950; Q628
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato T., Irie S., Krajewski S., Reed J.C.; "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein."; Gene 140:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis regulator Bcl-2.
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence ul)
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                adult rat brain.";
Neuroscience 61:165-177(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Castren E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 19-172 FROM N.A. MEDLINE=95059917; PubMed=7969891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovary: equine chorionic gonadotropin-mediated inhibition of granucell apoptosis is associated with decreased bax and constitutive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95129487; PubMed=7828536; Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.; "Expression of members of the bcl-2 gene family in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94193015; PubMed=8144041;
                                                                                                                                                                                                                                                                                                                                                                                                                 bcl-2 messenger RNA is localized in
                                                                                                                                                                                                                                                                                                                                                                                                                                               Lindholm D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A
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                                                                                                                  FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding the release of cytochrome c from the mitochondria and/or by binding the apoptosis-activating factor (APAP-1).

SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK are BC1-x(L). Heterodimerization with BAX requires intact BH1 and BH3 are applied to the state of the s
                                           domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity) SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T., Irie S., Krajewski S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGVNWGRIVAFFEFGGVMCVESVNREMSPLVDSIALWMTEYLNRHLHTWIQDNGGWDAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q62837;
SPECIFICITY: Expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
of the nuclear envelope and the endoplasmic reticulum PECIFICITY: Expressed in a variety of tissues, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q64032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berzaghi M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tzimagiorgis G., Thoenen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                       neurons of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.1e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                       the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the immature rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                       developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45;
                                                                                                                                                                                                            binding to
                                                                                                                                   and BH2
                                                                                                                                                           BAK and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    In PIM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity). It is proteinly cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity). It is similarity: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1). SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

ISIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

ISIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                  CONFLICT
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                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                             PROSITE; PS01260; PROSITE; PS50063;
                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50062;
                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
 10
                                                                     Local
                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal brain, expression is higher and localized in the neuroepithelium and in the cortical plate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).
DNREIVMKYIHYKLSORGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART 69
                           DTRALVADFVGYRLRQKGY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                       Pro; IPR003093; BH4.

Pro; IPR000712; Bcl_2.

PF00452; Bcl-2; 1.

PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q07817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L14680; AAA53662.1; -. U34964; AAA77687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S74122;
                                                                                                                                                                                                                                                                                                                                                                                               SM00337; BCL;
SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                          PS01259;
                                                                                                                                                                                                                                                                                                                                                     PS01258; BH2;
                                                                                                                                                                                                                                                                                                                                                                    PS01080; BH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002475; BCL2_family.
                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                     10
90
133
184
209
209
34
70
42
157
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1MAZ
                                                                                                                                                                                                                                                                                                             BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                        внз;
                                                                                                                                                                                                                                                                                                                                                                                 BCL2_FAMILY;
                                                                                                                                                     30
104
152
199
230
230
35
70
42
157
                                                                                                                             26622 MW;
                                                                    40.6%;
                                                                                                                                                                                                                                                                                              Mitochondrion; Phosphorylation
                                                        35;
                                                                                                                                  BH2.

POTENTIAL.

CLEAVAGE (BY CASPASES) (
PHOSPHORYLATION (BY PKC)
A -> R (IN REF. 1).
E -> G (IN REF. 2).
S -> Y (IN REF. 2).
L -> Q (IN REF. 2).
                                                                  Score 410; DB 1;
Pred. No. 1.8e-29;
                                                                                                                           E7688CB9071A872A CRC64;
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
                                                        62;
                                                                                 Length 236;
                                                                                                                                                                                             PKC) (BY
                                                     Indels
                                                                                                                                                                                                             (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                               SIMILARITY).
                                                     52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collaboration - 
L outstation -
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
BCL2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL2_MOUSE
P10417; P104
01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97277291; PubMed=9115213;
MEDLINE=97277291; PubMed=9115213;
Ito T., Deng X., Carr B., May W.S. Jr.;
"Bc1-2 phosphorylation required for anti-apoptosis function.";
J. Biol. Chem. 272:11671-11673(1997).
                                                                                                                                                                                                                                                                                                 Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;
"Reversible phosphorylation of Bcl2 following interleukin 3
bryostatin 1 is mediated by direct interaction with protein
phosphatase 2A*.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
Cell
     <del>:</del> :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/C; TISSUE=Liver; MEDLINE=87187643; PubMed=303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis regulator BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, 01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                   J. Biol. Chem. 273:34157-34163(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS TO 221-222
MEDLINE=92375724; Pul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.; "Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma."; cell 49:455-463(1987).
                                                                                                                                                                                                                                                                                                                                                                                       DEPHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eguchi Y., Ewert D.L., Tsujimoto Y.;
                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99069407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION BY PKC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolation and characterization of the chicken n a variety of tissues including lymphoid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                              Bcl-x(L). Heterodimerization with BAX requires intact domains, and is necessary for anti-apoptotic activity similarity). Also interacts with APAF-1 and RAF-1. SUBCELLULAR LOCATION: Outer mitochondrial membrane, in membrane of the nuclear envelope and the endoplasmic ralTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) a
                                                                                                                                              permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding the apoptosis-activating factor (APAF-1).

SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK are
are produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in a variety of tissues
DOMAIN: The BH4 domain is required for anti-apoptotic
                                                                                                                                                                                                                                 FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cell Regulates cell death by controlling the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=1508712;
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                                                                                                                                                                                                                                                                                                                                                                       Pubmed=9852076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF.
anti-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hcl-2 gene: expression
neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bc1-2
                                                                                                                                                                                 and/or by binding to
                                                                                    intracellular
                                                 reticulum and beta;
                                                                                                                                 BAD,
BH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236
 activity and
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                                                                                                                                  and
                                                                                                                                                                                                                                                    cells.
                                                                                                                                  ВН2
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cc -i- pTM: phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
cc anti-apoptotic activity. Growth factor-stimulated phosphorylation
cc on Ser-70 by PKC is required for the anti-apoptosis activity and
cc occurs during the G2/M phase of the cell cycle. In the absence of
cc growth factors, Bcl2 appears to be phosphorylated by other protein
cc kinases such as ERKs and stress-activated kinases.
cc pTM: proteolytically cleaved by caspases during apoptosis. The
cc cleaved protein, lacking the BH4 domain, has pro-apoptotic
cc cleaved protein, lacking the BH4 domain, has pro-apoptotic
cc activity, causes the release of cytochrome c into the cytosol
cc promoting further caspase activity.
cc similarity: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
cc similarity: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
cc similarity: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
cc similarity: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
cc similarity: BELONGS TO THE BCL-2 FAMILY.
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                        δÃ
                                                      Вb
                                                                              QΥ
                                                                                                                  Matches
                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50062; I
PROSITE; PS01080; I
PROSITE; PS01258; I
PROSITE; PS01259; I
                                                                                                                                                                                                                                Phosphorylation.
DOMAIN 10
DOMAIN 133
DOMAIN 184
TRANSMEM 209
SITE 34
MOD_RES 70
                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L31532;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                     VARSPLIC
70
                                                       10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E37332; E37332.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:88138; Bcl2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A25960; TVMSA1.
B25960; TVMSB1.
                                                                                     DTRALVADFVGYRLRQKGYVCGAG--
SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                                         DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00452; Bcl-2;
PF02180; BH4; 1.
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SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                             ; PS01080; BH1;
; PS01258; BH2;
; PS01259; BH3;
                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002475; BCL2_family.
IPR003093; BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                      Alternative
                           ----EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                                                                                                                         236
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1MAZ
                                                                                                                                                                                         ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL2_FAMILY;
                                                                                                                                                                                                                     104
152
199
230
35
70
                                                                                                                                                                                         26425 MW;
                                                                                                                                40.5%;
37.1%;
                                                                                                                                                                                                                                                                                                                                                    splicing; Transmembrane; Mitochondrion;
                                                                                                                  35;
                                                                                                                                Score 409; DB 1;
Pred. No. 2.2e-29;
                                                                                                                                                                                        PHOSPHORYLATION (BY PKC).

DAFVELYGPSWRPLEDDESWLSLKTILSLALVGACITLGAYL
GHK -> VGACLUE (IN ISOFORM BETA).

AA85EF6B0766BE0A CRC64;
                                                                                                                                                                                                                                                   POTENTIAL.
CLEAVAGE (BY CASPASES) (BY SIMILARITY).
                                                                                                                    Mismatches
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                                                                                                                     52;
                                                                                                                    Gaps
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BCL2_HUMAN STANDARD; PRT; 239 AA
BCL2_HUMAN STANDARD; PRT; 239 AA
P10415; P10416; Q16197; Q13842;
01-MAR-1999 (Rel. 10, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-BOLDEATON, CLEARY M.L., Smith S.D., Sklar J.; Cleary M.L., Smith S.D., Sklar J.; "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning analysis" and structural analysis of cDNAs for bcl-2 and "Cloning analysis" and "Cloning analysis" analysis of cDNAs for bcl-2 and "Cloning analysis" analysis of cDNAs for bcl-2 and "Cloning analysis" analysis and "Cloning analysis" and "Cloning analysis" and "Cloning analysis" analysis analysis analysis and "Cloning analysis" analysis analysis analysi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDLINE-88196071; PubMed-2834197;
Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in a varrey, adult and embryo.";
adult and embryo.";
- " "ids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eguchi Y., Ewert D.L., Tsujimoto Y., "Isolation and characterization of the chicken bcl-2 gene: expression "Isolation and characterization of the chicken bcl-2 gene: expression (A_{\rm chick})".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS TO 96; 110 AND 237.
MEDLINE=92375724; PubMed=1508712;
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"Analysis of the structure, transcripts, and protein products bcl-2, the gene involved in human follicular lymphoma.";
proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis regulator Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL MEDLINE=92096610; PubMed=1339299; Tanaka S., Louie D.C., Kant J.A., Reed J.C.; "Franka S., Louie D.C., Kant J.A., Reed J.C.; "Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-Hoddykin's lymphomas."; blood 79:229-237(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Alternative promoters and exons, somatic mutation of the Bcl-2-Ig fusion gene in lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goldman P., Korsmeyer S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 47:19-28(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=86259760; PubMed=3523487;
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apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J.
   Yin x.-M., Oltvai Z.N., Korsmeyer S.J.;
"BH1 and BH2 domains of Bcl-2 are required for inhibition
apoptosis and heterodimerization with Bax.";
                                                                                                                                                                                                          programmed
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                                                                                     wEDLINE=94239528; PubMed=8183370;
                                                                                                                           MUTAGENESIS
                                                                                                                                                                                                                                                                      Hockenbery D.,
                                                                                                                                                                                                                                                                                                     MEDLINE=91066924; PubMed=2250705;
                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION
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                                                                                                                                                                                                                is an inner mitochondrial mmed cell death.";
                                                                                                                                                                             nmed cell death.";
348:334-336(1990).
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                                                                                                                                                                                                                                                                         Nunez G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISOFORM ALPHA).
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                                                                                                                                                                                                                                                                               Milliman C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISOFORM ALPHA), AND VARIANTS NHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                            membrane protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                            Schreiber R.D., Korsmeyer S.J.;
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domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1.

-! SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

-! ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are produced by alternative splicing.

-! TISSUE SPECIFICITY: Expressed in a variety of tissues.

-! DOMAIN: The BH4 domain is required for anti-apoptotic activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto K., Ichijo H., Korsmeyer S.J.;
"BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal protein kinase pathway normally activated at G(2)/M.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruvolo P.P., Deng X., May W.S.;
"Phosphorylation of Bcl2 and regulation of apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20036804;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION BY ASK1/JNK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98057466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leukemia 15:515-522(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ueno K., Hardwick J.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLEAVAGE BY CASPASES, AND MUTAGENESIS
                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1.

PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.
                                                                                                                                                                                                                                                                                                                                                                                                     promoting further caspase activity.

DISEASE: Involved in follicular lymphoma (FL) (also known as type II chronic lymphatic leukemia) by a chromosomal translocation t(14:18)(q32:q21) which involves Bcl2 and immunoglobulin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity). PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the apoptosis-activating factor (APAF-1). SUBUNIT: Forms homodimers, and heterodimers with BAX, Bcl-x(L). Heterodimerization with BAX requires intact
                                                                                                                                                                                                                                                                                                                                                                                              regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell. Biol. 19:8469-8478(1999)
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EMBL; M13994; AAA51813.1; 7
EMBL; M13995; AAA51814.1; 7
EMBL; M14745; AAA35591.1; 7
EMBL; X06487; CAA29778.1; 7
EMBL; S72602; AAD14111.1; 7
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Best Local
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PIR; B29409;
PIR; A24428;
PIR; C37332;
PIR; D37332;
HSSP; Q07817;
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PROSITE;
190 QDNGGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00337; BCL; 1
SMART; SM00265; BH4; 1
                                                  139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane; Mitochondrion; Phosphorylation; Chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00452; Bc1-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003093; InterPro; IPR000712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 151430;
                                                                                                                                                                                  70
                                                                                                                                                                                                                                                           10 DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART 69
                                                                                                                                                                                                                                                                                                         ; A29409; TVHUA1.
; B29409; TVHUB1.
; A24428; TVHUBC.
; C37332; C37332;
; D37332; D37332.
                                           HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                  FATVVEBLFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWNTEVLNRHLHTWI
                                                                                                                         FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWI 138
                                                                                                                                                                         SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50062; BCL2_FAMILY; 1
PS01080; BH1; 1.
; PS01258; BH2; 1.
; PS01259; BH3; 1.
; PS01259; BH3; 1.
; PS01260; BH4_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
93
136
187
212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                    -----GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 I
26266 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
64
145
                                                                                                                                                                                                                                                                                                                                                                      40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-A: NO HETERODIMERIZATION WITH BAX AND LOSS OF ANTI-APOPTOTIC ACTIVITY.

W-A: NO HETERODIMERIZATION WITH BAX AND LOSS OF ANTI-APOPTOTIC ACTIVITY.

I -> F (IN REF. 4).
P -> T (IN REF. 3).
R -> C (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                      Score 408.5; DB
Pred. No. 2.5e-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
GHK -> VGASGDVS (IN ISOFORM BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
CLEAVAGE (BY CASPASE-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_000829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3C49F2B714DC9CCB CRC64;
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO EFFECT ON CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABOLISHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _000828
                                                                                                                                                                                                                                                                                                                                                                                             ٠.
                                                                                                                                                                                                                                                                                                                                                                                             Length 239;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CASPASE-3.
BY CASPASE-3
                                                                                                                                                                                                                                                                                                                                                    55;
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                  5
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us-09-155-327e-9.rsp

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RESULT
BCL2_CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Apoptosis regulator Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9JJV8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES. MEDLINE-21092839; PubMed-11181062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCL2_CRILO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 275:899-903(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomicic M.T., Christmann M., Kaina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20431763; PubMed=10973819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 281:404-408(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tomicic M.T., Kaina B.; "Hamster Bcl-2 protein is cleaved in vitro and in cells by
                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity). Also interacts with APAF-1 and RAF-1 (By Similarity). SUBCELULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activities either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity). BAK and SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and RH2 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caspase-3."
                                                                                                                                                                                                                                                                                                                                                                                 cleaved protein, lacking the BH4 domain, has pro-apopt activity, causes the release of cytochrome c into the promoting further caspase activity.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with
                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
   AJ271720; CAB92245.1; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteolytically cleaved by caspases during apoptosis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                             institutions as long as its content
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                                                                                                                                                                         Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as pro-apoptotic
c into the cytos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytosol
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Best Local :
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InterPro; IPR003093; BH4.
InterPro; IPR000712; Bcl__
InterPro; IPR000712; Bcl__
Pfam; PF00452; Bcl-2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50062; BCL2_FAMILY; PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00337; BCL; SMART; SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.

-:- SUBCELLULAR LOCATION: Membrane-bound (Potential).

-:- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.

-:- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
                                                                                                                                                                                 "Cloning, characterization and expression of two Xenopus cell-survival genes.";
Gene 158:171-179(1995).
                                                                                                                                                                                                                                                              Cruz-Reyes J., Tata J.R.;
                                                                                                                                                                                                                                                                                          MEDLINE=95331613; PubMed=7607538;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptosis regulator R11 (XR11)
                                                                                                                                                                                                                                                                                                                        TISSUE=Head
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 399; DB Pred. No. 1.7e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 AA
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Search completed: June 10, 2002, 10:32:13 Job time: 346 sec
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Best Local Similarity
Matches 81; Conserv
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HSSP; Q07817; 1MAZ.
InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
InterPro; IPR003093; BH4.
InterPro; IPR000712; BCl_2.
Pfam; PF00452; BCl_2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00355; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                       184 RLLTI-VMLTGVFAL 197
                                                                                                                                                      124 VESANKEMTDILPRIVQWMVNYLEHTLQFWMQENGGWEAFVGLYGKNAAAQSRESQERFG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis; Transmembrane.
                                                                                                                                                                              108 AESVNKEMEPLVGQVQDWWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--G 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                           166 NWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                              64 EATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRDGTNWGRIVAFFSFGRALC 123
                                                                                                                                                                                                                                               48 AAGDEFETRERRTESDLAAQLHVTPGSAQQRETQVSDELEQGGDNWGRLVAEFVFGAALC 107
                                                                                                                                                                                                                                                                                                                                       10 TRALVADEVGYRLRQKGYVC-------GAGPGEGPAADPLHQAMR 47
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                                                                                                                                                                                                                                                                                                    SRDLVEKFVSKKLSQ-NEACRKFSNNPNPMPYLMEPSTSERPGEGATQGIVEEEVLQALL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 120 BH1.
152 167 BH2.
181 198 POTENTIAL.
204 AA; 23379 MW; 3BFC6BE6DDA4CA03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                         36.3%; Score 366; DB 1; Length 204;
41.5%; Pred. No. 1.2e-25;
tive 25; Mismatches 63; Indels :
                                                                                                                                                                                                                                                                                                                                                                           Indels 26; Gaps
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OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_rvirus:*
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sp_plant:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	14	13	12	11	10	9	8	7	0	ر ن	4	w	2	٠ +	-	Result No.
347	369.5	371.5	371.5	395	397	399.5	401	401	425.5	428.5	432.5	436.5	161	1 6	1002	Score
34.4	36. 56.	36.8	36.8	39.1	39.3	39.6	39.7	39.7	42.2	42.5	42.9	43.3	/0.0	3 1	99.3	Query Match L
219	204	235	188	236	238	180	217	180	233	233	233	200) ·	170	193	Length DB
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Q99n36 mus musculu	Q90zh2 xenopus lae	OSCIPTION CANTED	1100	092310 CIICECUIUS	Canada artacitamina	Cantas of Xnd67	Capital poe tailing		Contact to the terms	Compact out totors	Ognla? sus scrofa	035844 mis musculu	Ogmyw4 orvetolagus	09cyw5 mus musculu	088996 rattus norv	Description

Query Match

99.3%; Score 1002;

DB 11; Length 193;

45	44	43	42	41	40	9	ა 8	37	36	ω 5	34	ω W	32	u	30	29	28	27	26	25	24	23	22	21	20	19	18	17
119	121	121.5	124.5	127.5	129.5	130	136	137.5	137.5	137.5	138.5	141	141.5	142	142	144	145	147.5	148.5	154	157.5	162	163	165.5	175.5	177.5	182	187
11.8	12.0	12.0	12.3	12.6	12.8	12.9	13.5	13.6	13.6	13.6		14.0	14.0	14.1	14.1	14.3	14.4	14.6	14.7	15.3	15.6	16.1	16.2	16.4	17.4	•	18.0	
300	174	91	91	331	330	162	114	213	213	213	213	255	179	212	211	177	149	179	218	173	163	58	235	125	221	192	170	209
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Q9V9C8	Q9W6F2	Q923W6	Q923W5	P97287	Q9Z1P3	Q9DH00	Q9NR76	Q9DGJ5	21815	Q9UL32	035425	Q919N3	Q9EIF2	Q9UMX3	THOMEO	Q90ZN1	Q9GMG7	Q9NYG7	Q9N754	Q9JKL3	Q9MZS6	Q9RIB3	Q967D2	Q9H1R5	Q98U13	Q919N4	Q9WUI5	Q9JK59
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ALIGNMENTS

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088996
                                         InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; BC1_2.
InterPro; IPR000712; BC1_2.
InterPro; IPR0003093; BH4.
Pfam; PP00452; BC1-2; 1.
Pfam; PP00452; BC1-2; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PR0SITE; PS01080; BH1; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     088996;
01-NOV-1998 (TIEMBLrel. 08, Created)
01-NOV-1998 (TIEMBLrel. 08, Last sequence update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
                                                                                                                                                                                 Hamner S., Skoglosa Y., Lindholm D.;
"Differential expression of bcl-w and bcl-x messenger RNA in the developing and adult rat nervous system.";
Neuroscience 91:673-684(1999).
EMBL; AF096291; AAC64200.1;
HSSP; Q07817; IMAZ.
                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            088996
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
MEDLINE-99292146; PubMed-10366024;
                                                                                                                                                                                                                                                                                                                                                                                           BCL-W
   SEQUENCE
             PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
    193 AA;
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      20820 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
      36D6742F4529AFB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 AA.
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Local Similarity

99.0%;

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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashiraki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
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                                                                                                                           MGD: MGI:108052; Bc1212.
InterPro; IPR002475; BCL2_family.
InterPro; IPR00712; BcL2.
InterPro; IPR003093; BH4.
INTERPRO; INTERPRO; BH4; INTERPRO; INTERP
   PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS50063; BH4_2; 1.
SEQUENCE 178 AA; 19147 MW; E2
                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK013244; BAB28740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9CYW5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=EMBRYO; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                      Q07817; 1MAZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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1; Mismatches 1;
E2D4C3F79528E9D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 AA
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                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                        PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01250; BH4_1; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;
         186
                           142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00452; Bc1-2; 1. Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AY005131; AAF88137.1; -.
                                                                126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Cranıata; ver
Mammalia; Eutheria; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002475; BCL2_family InterPro; IPR000712; Bcl_2. InterPro; IPR003093; BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryotolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P53563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Rabbit Bcl-X."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9MYW4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9MYW4
                                                                                 82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWWVAYLETRLADWIHSS 141
                                                                                                                                 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 QVQDWMVAYLETRLADWIHSSGGWVRSSQL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 QVQDWMVAYLETRLADWIHSSGGWAEFTAL 150
                                                                                                                                                                                                                                       Local Similarity 41.9 es 93; Conservative
                                                                                                                                                                         6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTGPEMETPSAINGNPAWHPADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FSDLAAQLHYTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FSDLAAQLHYTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MATPASTPDTRALVADEVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
                                                       VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMEVLVSRIAAWMATYLNDHLEPWIQEN 185
                                                                                                                NGATGHSSSLDAREVIPMTAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robertson L., James E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                    43.3%; Score 436.5;
41.5%; Pred. No. 2e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.0%;
96.0%;
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Pred. No. 2e-59;
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 AA
                                                                                                                                                                                                                                                     2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 178;
                                                                                                                                                                                                                                                                DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus
                                                                                                                                                                                                                               57; Indels 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
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Best Local S
Matches 93
                                          Q9N1A2 PRELIMINARY;
Q9N1A2;
Q9N1A2;
Q1-OCT-2000 (TrEMBLrel. 15, C
Q1-OCT-2000 (TrEMBLrel. 15, L
Q1-DEC-2001 (TrEMBLrel. 19, L
ANTI-APOPTOTIC REGULATOR BCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O35844; PRELIMINARY;
O35844;
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel Bc1-x isoform connected apoptosis in T cells."; Immunity 7:629-639(1997).
EMBL; U51278; AAC53459.1; --
HSSP; P53563; 1AF3.
  Eukaryota;
Mammalia;
                        Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=B6/CBA; TISSUE=THYMUS; MEDLINE=98051053; PubMed=9390687; Yang X.-F., Weber G.F., Cantor H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
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                                                                                                                                                            185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ); MGI:88139; Bcl21.
cerpro; IPR002475; Bcl.2_family.
cerpro; IPR000712; Bcl.2.
cerpro; IPR003093; BH4.
im; PF00452; Bcl-2; 1.
im; PF02180; BH4; 1.
                                                                                                                                                                      SGGWAEFTALYGDGALEEARRLREG--NWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                  QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                   RALVADFVGYRLRQKGY-----
                                                                                                                                                                                                      QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                                                                                                                                                                                                                                        CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                             RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
                                                                                                                                                          NGGWDTFVDLYGNNAAAESRKGKEGFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                            93;
                                                                                                                                                                                                                                                                                                                                                                                                                               PS50062; BCL2_FAM:
PS01080; BH1; 1.
PS01258; BH2; 1.
PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                PS50063;
                                                                                                                                                                                                                                                                                                                                                                                                                      PS01260;
 ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                ; BH4_1; 1.
; BH4_2; 1.
a; 26033 MW;
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BH1; 1.
Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                    42.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05,
19,
                                              BCL-XL.
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                                                       Last sequence update)
Last annotation updat
                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4.4e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                        update)
                                                                                                                                                                                                                                                                                                                                          56;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                             Length
  Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulates
                                                                                                                                                                                                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                   ----V 28
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7 1D 297
1D 29
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Best Local
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InterPro; IPR002475; BCL2,
InterPro; IPR000712; Bcl_
InterPro; IPR0000713; BH4
InterPro; IPR003093; BH4
Pfam; PF00452; Bcl-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                Q9MZS7;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
BCL-X LONG PROTEIN.
Ovis aries (Sheep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002475; BC InterPro; IPR000712; BC InterPro; IPR000093; BH InterPro; IPR003093; BH Pfam; PF00452; BC1-2; 1 Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                       TISSUE-OVARY;

Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi
"Bcl-x in the sheep ovary.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ

EMBL; AF164517; AAF89532.1;

HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9MZS7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee T.L., Canty J.M.;
"PCR Cloning of a Porcine bcl-xL cDNA from Heart.";
"DCR Cloning of a Porcine bcl-xL cDNA from Heart.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF216205; AAF33212.1; ...
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; Q07817; 1MAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 RALVADFVGYRLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00337; BCL; 1.
SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; PS50062; BCL2_FAMILY; 1

2; PS01080; BH1; 1.

2; PS01258; BH2; 1.

2; PS01259; BH3; 1.

2; PS01259; BH3; 1.

3; PS01260; BH4_1; 1.

2; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                 ; BCL2_family.; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.5%;
                                                                              BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26047 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         вн4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 428.5; DB b;
Pred. No. 9.9e-30;
Prematches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2FA312818B25E17D CRC64;
                                                                                                                                                                                                                                                              Scaramuzzi R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233
                                                                                                                                                                                                                databases
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                                                                                                                                                                                                                                                                 Carter
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Best L
                                                                                                     Matches
                                                                                                                               Query Match
Best Local
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PROSITE; PS50062; BCL2_FAMILY; 1

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01259; BH3; 1.

PROSITE; PS01250; BH4_1; 1.

PROSITE; PS01260; BH4_2; 1.

PROSITE; PS0063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BDD5;
                                                                                                                                                                                                                            NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of the bovine bcl-xL gene and related pseudogenes."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF245488; AAK31307.1; -.

EMBL; AF245489; AAK31308.1; -.

HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                    PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amills M., Bouzat J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
  38
                          44 QAMRAAGDEFETRERRTESDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQEN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGWAEFTALYGDGALEEARRIRE--GNWASVRTVLTGAVALGAL 183
  QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGATGHSRSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELYVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESDMETPSAINGNPSWHLADSPAV
                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                               180
180 AA;
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.
                                                                                                                                                                                                                               180
20062 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26134 MW;
                                                                                                                          39.7%;
                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                            Score 401; DB 6;
Pred. No. 1.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 425.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                 95DC436F95DABDA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             012BFA1382762915 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8e-29;
hes 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                       45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6;
                                                                                                                                                  Length 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                     2;
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141
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     97
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Q9BDX7
ID Q9BDX7
AC Q1
DT 01
DT 01
DT 01
DT 02
DT 02
DT 02
DT 03
DT 04
DT 04
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Best Local
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF133282; AAK15455.1; -.
EMBL; AF133281; AAK15455.1; JOINED.
HSSP; P53563; 1AF3.
HSSP; P53563; 1AF3.
                                                                                               O9BDX7.

O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q99N35;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
B-CELL LEUKEMIA/LYMPHOMA X (FRAGMENT).
  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantla; Pec
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002475; BCL2_family.
InterPro; IPR000711; Bcl_2.
Pfam; PF00452; Bcl_2; 1.
SMART; SM00337; BCL; 1.
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"Novel cDNA structure and genomic organization of apoptosis regulatory gene Bcl-x-gamma.";
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                                                                                                                                                                                                                                                                                                                                                                                                                        E--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG 131
                                                                                                                                                                                                                                                                                                                                                                       ERFNRWFLTGMTVAGVVLLGSL
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PS01080; BH1; 1.
PS01258; BH2; 1.
PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 AA;
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                                                                                                                                                                                                                                          PRELIMINARY;
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Pred. No. 2.3e-27;
                                                                                                                                                                                                                                          PRT;
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                             Ruminantia; Pecora;
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                                                      Euteleostomi;
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Best Local :
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Best Local
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01-DEC-2001
01-DEC-2001
01-DEC-2001
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Interpro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
SMART; SM00337; BCL; 1.
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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=21299061; PubMed=11406282;
Chen M.-C., Gong H.-Y., Cheng C., Wang J.-P., Hong J., Wu J.

"Cloning and characterization of zfBLP1, a Bcl-XL homologue zebrafish, Danio rerio(1).";
EMBL; AF317837; AAK81706.1;
SEQUENCE 238 AA; 26253 MW; 6E58394933EEFDDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7955
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| : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                   RELVVFFIKYKLSQRNYPCNHIGLTEDTNRTDGAEENGEGAAGATTLVNGTMNRTNASST
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(TremBLrel. 19, Last seq
(TremBLrel. 19, Last ann
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47.1%;
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                                                                                                                                                                                                                              39.3%;
35.7%;
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                                                                                                                                                                                                       29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                            Score 397; DB 13;
Pred. No. 5.7e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 399.5; DB 6; Pred. No. 2.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                    -AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                      DB 13;
                                                                                                                                                          --GAG---
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                                                                                                                                                                                                         62;
                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                        238;
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                                                                                                                                                                                                       Gaps
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RESULT
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                                                                                                                                                                                                                                                                             RESULT
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Best Local
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01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
B-CELL LYMPHOMA PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lai D.Z., Chen W., Wang H.T.;
"Construction of a robust CHO cell line for biopharmaceutical use.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF404339; AAK92201.1; -
SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8B8 CRC64;
                                                                                             ACL: A SCIPA (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Metazoa; Chordata;

Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q923R6
MEDLINE-20350651; PubMed-10894153;
Rucker E.B. III, Dierisseau P., Wagner K.U., Garrett L.,
Wynshaw-Boris A., Flaws J.A., Hennighausen L.;
"Bcl-x and Bax regulate mouse primordial germ cell survi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10030;
                                                                                                                                                                                                                                 Q9QWX2;
                                                                                                                                                                                                                                              Q9QWX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 QSQGGWERFAEIFGKDAAAESRKSQESFKKWLFAGMTLLTG-----VVVVGGLIAQK 236
                                                             SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                    BCL-X (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSGGWAEFTALYGDGALEEARRLREG--NWA-SVRTYLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                        GGWDAFVELYG----PSVRPLFDFSWLSLXTLLNLAL-VGACITLGTYLGHK
                                                                                                                                                                                                                                                                                                                                                     GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK
                                                                                                                                                                                                                                                                                                                                                                                    VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                                                                                                                                                                                                                                                                                                  VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIESFQPESNPTPAVHRDMAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTRALVADFVGYRLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                               SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                 PRELIMINARY;
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Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                   Created)
                                                                                                                                                                                      Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 395; DB 11;
Pred. No. 8.5e-27;
3; Mismatches 66
                                                                                                                                                                                                                                                   PRT;
                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
   primordial germ cell survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
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Best Local (
MGD; MGI:88139; Bc121.
InterPro; IPR002475; BCL2_family.
InterPro; IPR007712; Bcl_2.
InterPro; IPR003093; BH4.
InterPro; IPR003093; BH4.
Pfam; PF00452; Bcl_-2; 1.
Pfam; PF00452; Bcl_-1.
SMART; SM00337; BCL; 1.
SMART; SM00337; BCL; 1.
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SMART; SM00337; BCL; 1.

SMART; SM00265; BH4; 1.

PROSITE; PS50062; BCL2_FAMILY; 1

PROSITE; PS01080; BH1; 1.

PROSITE; PS01259; BH3; 1.

PROSITE; PS01250; BH4_1; 1.

PROSITE; PS01260; BH4_2; 1.

PROSITE; PS0063; BH4_2; 1.

PROSITE; PS50063; BH4_2; 1.

RON_TER 188 188

SEQUENCE 188 AA; 21126 MW; 4
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InterPro: IPR000712; Bcl_2:
InterPro: IPR000712; BH4.
Pfam; PF00452; Bcl-2; 1.
Pfam; PF00452; Bd1-2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                 WEDLINE=98051053; PubMed=9390687; Yang X.-F., Weber G.F., Cantor H. "A novel Bcl-x isoform connected apoptosis in T cells."; Immunity 7:629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O35843
O35843;
O1-JAN-1998
O1-JAN-1998
O1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=B6/CBA; TISSUE=THYMUS;
                                                                                                                                                                                                               EMBL; U51277; AAC53458.1; -. HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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MGD; MGI:88139; Bcl21.
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Mol. Endocrinol. 14:1038-1052(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTESDLAAQLHYTPGSAQQRFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF088904; AAC72232.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78;
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42.4%; Pred. No. 7.1¢
tive 17; Mismatches
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Bcl_2.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                the T cell receptor regulates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
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RESULT 14
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Best Local Similarity
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Best Local :
                                                                                                                                                                     SMART; SM00337; BCL; 1.
SMART; SM00255; BH4; 1.
PROSITE: PS50062; BCL2_FAMILY; 1
PROSITE: PS50063; BH1; 1.
PROSITE: PS50063; BH4_2; 1.
NON_TER 188 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9H1R6;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                            InterPro; IPR003093; BH4. Pfam; PF00452; BC1-2; 1. Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                 InterPro; IPR002475; BCL2_family
InterPro; IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                                                         EMBL; AL160175; CAC
HSSP; Q07817; 1LXL
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TYEMBLIEL. 16, Created)
01-MAR-2001 (TYEMBLIEL. 16, Last sequence update)
01-DEC-2001 (TYEMBLIEL. 19, Last annotation update)
BA243J16.1.1 (BCL2-LIKE 1 (ISOFORM 1)) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                Submitted (MAY-2001)
                                                                                                                                                                                                                                                                                                                                              Brown A.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9H1R6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 NGGW 188
66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 SGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                       11 RALVADFVGYRLRQKGY-----
                      29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 RALVADFVGYRLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                             RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS50062; 1
PS01080; 1
PS01259; 1
PS01260; 1
PS50063; 1
235 AA;
                                                                                                                                                           188 AA;
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                    CAC10003.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; BH3; 1.
; BH4_1; 1.
; BH4_2; 1.
A; 26122 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL2_FAMILY; 1.
                                                                                                                                                          21029 MW; 7074B6095145C324 CRC64;
                                                                                                           36.6%; Score 369.5; 42.4%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.8%;
                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 371.5; DB Pred. No. 9.5e-25
                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649D914C2D5378F6 CRC64;
                                                                                                           No. 1.1e-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    À
                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                     Length
                                                                                              Indels
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                                                                                                                      188;
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RESULT
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Search completed: June 10, 2002, 10:31:19 Job time: 392 sec
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                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 36.5%; Score 368; DB 13; Length 204; Best Local Similarity 42.3%; Pred. No. 1.6e-24; Matches 82; Conservative 24; Mismatches 64; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q90ZH2 PRELIMINARY;
Q90ZH2;
O1-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-DEC-2001 (TrEMBLrel. 19, L
BCL-XL.
BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakajima K., Yaoita Y.; "Muscle cell death occurs in the regressing tail of tadpole by suicide mechanism."; Suicide mechanism."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB055494; BAB62748.1; -. SEQUENCE 204 AA; 23189 MW; 1BEF1B904E29D84A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 NGGW 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 SGGW 144
                                                                                                                                                                                                                                                                                                                                                                                      109 ESVNKEMEPLVGQVQDWNVAYLETKLADWIHSSGGWAEETALYGDGALEEARKLKE--GN 166
                                                                                                                                                                                                                                                                     167 WASVRTVLTGAVAL 180
                                                                                                                                                                                             185 LLTI-VMLTGVFAL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 ATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRDGTNWGRIVAFFSFGRALCV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 TRALVADEVGYRLRQ-----KGYVCGAGPGEGP----AADPLHQAMRA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 SRDLVEKFVSKKLSQNEACRKFSNNPQPNAISNGTSTSERPGEGATQGIVEEEVLQALLE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGDEFETRERRTESDLAAQLHVTPGSAQQRETQVSDELFQGGPNWGRLVAFFVFGAALCA 108
                                                                                                                                                                                                                                                                                                                                          ESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFGR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
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